

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 14, 2004, 15:52:50 ; Search time 1784.1 Seconds
(without alignments)
8323.656 Million cell updates/sec

Title: US-09-759-112a-5

Perfect score: 363

Sequence: 1 caggttactctgaagagtc.....cctcagtcacgcgtctctca 363

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hcg.*

3: gb_in.*

4: gb_cm.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

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10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rod.*

36: em_htg_mam.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match %	Length	DB	ID	Description
1	316.6	87.2	360	10	MMHCV3	X75097 M. musculus
2	314.6	86.7	420	10	AY090903	AX090903 Mus muscu
3	311.8	85.9	426	6	AX458152	AX458152 Sequence
4	305.4	84.1	360	10	MMU22977	U22977 Mus musculu
5	305.4	84.1	360	10	MMU22979	U22979 Mus musculu
6	305.4	84.1	360	10	MMU22994	U22994 Mus musculu
7	303.8	83.7	360	10	MMU22992	U22992 Mus musculu
8	303.6	83.6	366	6	E07584	E07584 Gene fragme
9	300.6	82.8	360	10	MMU22981	U22981 Mus musculu
10	300.6	82.8	360	10	MMU23010	U23010 Mus musculu
11	300.6	82.8	360	10	MMU23013	U23013 Mus musculu
12	300.6	82.8	361	10	MMU23004	U23004 Mus musculu
13	299.6	82.5	360	10	MMU22999	U22999 Mus musculu
14	299.2	82.4	738	6	E07990	E07990 DNA encodin
15	299.2	82.4	738	6	I45910	I45910 Sequence 6
16	298.6	82.3	358	10	MMU23002	U23002 Mus musculu
17	295.8	81.5	360	10	MMU22983	U22983 Mus musculu
18	295.8	81.5	360	10	MMU22984	U22984 Mus musculu
19	295.8	81.5	360	10	MMU23005	U23005 Mus musculu
20	295.8	81.5	360	10	MMU23009	U23009 Mus musculu
21	294.4	81.1	360	10	MMU22997	U22997 Mus musculu
22	294.2	81.0	366	10	MMIGMSMJ	X53097 Mouse mRNA
23	293.8	80.9	358	10	MMU23000	U23000 Mus musculu
24	293.4	80.8	359	10	MMU23007	U23007 Mus musculu
25	293.2	80.8	438	10	S75897	S75897 Ig VH-19g h
26	291.4	80.3	365	10	MMU22929	U22929 Mus musculu
27	291	80.2	418	6	AR026944	AR026944 Sequence
28	290.4	80.0	348	10	MMHCV3	X75098 M. musculus
29	289.8	79.8	365	10	MMU22905	U22905 Mus musculu
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33	289.8	79.8	365	10	MMU22956	U22956 Mus musculu
34	289.8	79.8	365	10	MMU22957	U22957 Mus musculu
35	289.8	79.8	195281	10	AC073939	AC073939 Mus muscu
36	289.6	79.8	360	10	MMU22988	U22988 Mus musculu
37	289.2	79.7	326	10	MMU22986	U22986 Mus musculu
38	288.4	79.4	363	10	S62427	S62427 anti-paraqu
39	288.2	79.4	365	10	MMU22955	U22955 Mus musculu
40	287.8	79.3	1410	10	MMU421677	AJ421677 Mus muscu
41	285.6	78.7	357	10	S63186	S63186 Ig VH-anti-
42	285	78.5	318	10	MMU22990	U22990 Mus musculu
43	285	78.5	330	10	MMU22975	U22975 Mus musculu
44	282.8	77.9	353	10	MMU22995	U22995 Mus musculu
45	281.8	77.6	365	10	MMU22907	U22907 Mus musculu

ALIGNMENTS

RESULT 1

MMHCV3

LOCUS

DEFINITION

MMHCV3

M. musculus (A.S.W)

360 bp

mrna

linear

ROD 23-FEB-1994

antibody heavy chain variable

region.

X75097

GI:414165

antibody; variable region; VH region.

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 360)

Nonetier M., Lozman M.J., Novick K.E. and Aris, J.P.

AUTHORS

TITLE

Molecular analysis of mercury-induced antinuclear antibodies in

RESULT 2					
AY090903					
LOCUS	AY090903	420 bp	mRNA	linear	ROD 17-APR-2002
DEFINITION	Mus musculus clone GN-2-M4 monoclonal anti-alpha-1,3-galactosyltransferase IgM heavy chain mRNA, partial cds.				

[illegible]


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QY 361 TCA 363
Db 358 TCA 360

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MMU22992
LOCUS Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
DEFINITION clone 45-26h, partial cds.
ACCESSION U22992
VERSION U22992.1 GI:780586
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 360)
AUTHORS Young,D. and Kearney,J.F.
TITLE Sequence analysis and antigen binding characteristics of Ig SCID
JOURNAL Int. Immunol. 7 (5), 807-819 (1995)
MEDLINE 96053543
PUBMED 7547707
REFERENCE 2 (bases 1 to 360)
AUTHORS Young,D.C.
TITLE Direct Submission
JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
Houston, TX 77030, USA
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Best Local Similarity 91.7%; Pred. No. 2.4e-87;
Matches 333; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY 1 CAGGTACTCTGAAGAGTCTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCAGTCTG 60
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Db 61 ACTTGTCTTTCTCGGGTTTTCAGTACACATTTCTGGTATGGGTGTGAGCTGGATTCGT 120
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Db 301 GTCTCTTAAGTGTGGACACTCGAGATACGCCACATACACTACTGTGTCGAAGG 360
QY 361 TCA 363
Db 358 TCA 360

RESULT 8
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LOCUS Gene fragment coding the variable region in the heavy chain.
DEFINITION E07584
ACCESSION E07584
VERSION E07584.1 GI:2175719
KEYWORDS JP 1994141885-A/1.
SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE 1 (bases 1 to 366)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Eda,Y., Nagatomi,K., Shiosaki,K., Maeda,H., Kurumi,K. and
Tokiyoshi,Y.
TITLE MONOCLONAL ANTIBODY
JOURNAL Patent: JP 1994141885-A 1 24-MAY-1994;
COMMENT CHEMO SERO THERAPEUT RES INST
OS Mus sp. (mouse)
PN JP 1994141885-A/1
PD 24-MAY-1994 JP 1992322476
PF 05-NOV-1992 JP 1992322476
PI ED A YASUYUKI, NAGATOMI KIYOSHI, SHIOSAKI KOUICHI, PI MAEDA
HIROAKI,
PI KURUMI KAZUHIKO, TOKIYOSHI YUKIO
PC C12P21/08.C07K15/28//C12N15/06.C12N15/13.C12N15/62.G01N33/569,
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CC strandedness: Double;
CC topology: Linear;
FH Key Location/Qualifiers
FT source 1..366
FT /organism="Mus sp."
FT /db_xref="taxon:10095"
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Best Local Similarity 91.3%; Pred. No. 2.8e-87;
Matches 334; Conservative 0; Mismatches 29; Indels 3; Gaps 1;

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QY      241 TTCTCTCAAGTACCAAGTGTGGACACTGAGATAGTGCACATATCTGTGCTCGAAGG 300
Db      241 TTCTCTCAAGTACCAAGTGTGGACACTGAGATAGTGCACATATCTGTGCTCGAAGG 300
QY      301 G---TCTCTTAACCTGCTATGCTATGGAAGTCAAGGAACTTCAGTCAACCTC 357
Db      301 GTCTCTTAAGTAACTCCGATTTATGACCACTGGGGTCAAGGAACCTCAGTCAACCTC 360
QY      358 TCCTCA 363
Db      361 TCCTCA 366

RESULT 9
MMU22981
LOCUS   Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
        clone 45-13h, partial cds.
DEFINITION
ACCESSION U22981
VERSION   U22981.1 GI:780564
KEYWORDS
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
REFERENCE 1 (bases 1 to 360)
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE     Young,D. and Kearney,J.F.
          Sequence analysis and antigen binding characteristics of Ig SCID
          Ig+ mice
JOURNAL   Int. Immunol. 7 (5), 807-819 (1995)
MEDLINE   96053543
PUBMED    7547707
REFERENCE 2 (bases 1 to 360)
AUTHORS   Young,D.C.
TITLE     Direct Submission
JOURNAL   Submitted (17-MAR-1995) David C. Young, University of Texas Health
          Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
          Houston, TX 77030, USA
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QY      361 TCA 363
Db      358 TCA 360

RESULT 10
MMU23010
LOCUS   Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
        clone 45-6h, partial cds.
DEFINITION
ACCESSION U23010
VERSION   U23010.1 GI:780622
KEYWORDS
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
REFERENCE 1 (bases 1 to 360)
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE     Young,D. and Kearney,J.F.
          Sequence analysis and antigen binding characteristics of Ig SCID
          Ig+ mice
JOURNAL   Int. Immunol. 7 (5), 807-819 (1995)
MEDLINE   96053543
PUBMED    7547707
REFERENCE 2 (bases 1 to 360)
AUTHORS   Young,D.C.
TITLE     Direct Submission
JOURNAL   Submitted (17-MAR-1995) David C. Young, University of Texas Health
          Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
          Houston, TX 77030, USA
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          Query Match 82.8%; Score 300.6; DB 10; Length 360;

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Matches 331; Conservative 0; Mismatches 29; Indels 3; Gaps 1;

QY 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGACAGCCCTCCAGACCCCTCAGTCTG 60
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QY 241 TTCCTCAAGATCACCAGTGTGGACACTCGAGATACCTGCCACATACCTACTGTCTCGAAG 300
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QY 361 TCA 363
Db 358 TCA 360

RESULT 11
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LOCUS Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
DEFINITION clone 45-8h, partial cds.
ACCESSION U23013.1 GI:780628
VERSION 1
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 360)
AUTHORS Young,D. and Kearney,J.F.
TITLE Sequence analysis and antigen binding characteristics of Ig SCID
JOURNAL Int. Immunol. 7 (5), 807-819 (1995)
MEDLINE 96053543
PUBMED 7547707
REFERENCE 2 (bases 1 to 360)
AUTHORS Young,D.C.
TITLE Direct Submission
JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
Houston, TX 77030, USA
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BASE COUNT 83 a 99 c 87 g 91 t
ORIGIN
Query Match 82.8%; Score 300.6; DB 10; Length 360;
Best Local Similarity 91.2%; Pred. No. 2.6e-86;
Matches 331; Conservative 0; Mismatches 29; Indels 3; Gaps 1;
QY 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGACAGCCCTCCAGACCCCTCAGTCTG 60
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QY 61 ACTTGTCTCTTCTCTGGGTTTTCACGTAGACACTTCTGGTATGGGTGAGTGGATTCGA 120
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RESULT 12
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LOCUS Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
DEFINITION clone 45-3h, partial cds.
ACCESSION U23004
VERSION U23004.1 GI:780610
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 361)
AUTHORS Young,D. and Kearney,J.F.
TITLE Sequence analysis and antigen binding characteristics of Ig SCID
JOURNAL Int. Immunol. 7 (5), 807-819 (1995)
MEDLINE 96053543
PUBMED 7547707
REFERENCE 2 (bases 1 to 361)
AUTHORS Young,D.C.
TITLE Direct Submission
JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
Houston, TX 77030, USA
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CDS

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GSTFDYWGQGTTLTVSS"
BASE COUNT 83 a 99 c 88 g 91 t
ORIGIN

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Query Match 82.8%; Score 300.6; DB 10; Length 361;
Best Local Similarity 91.2%; Pred. No. 2.6e-86;
Matches 331; Conservative 0; Mismatches 29; Indels 3; Gaps 1;

QY 1 CAGGTACTCTGAAGAGTCTGGCCCTGGGATATTGCAGCCCTCCAGACCCCTCAGTCTG 60
DB 1 CAGGTACTCTGAAGAGTCTGGCCCTGGGATATTGCAGTCTCCAGACCCCTCAGTCTG 60
QY 61 ACTTGTTCTTTCTCTGGGTTTTCACCTGAGCATTCTGGTATGGTGTGAGCTGGATTCTG 120
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QY 361 TCA 363
DB 358 TCA 360

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RESULT 13
MMU22999
LOCUS Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
DEFINITION clone 45-2h, partial cds.
ACCESSION U22999
VERSION U22999.1 GI:780600
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 360)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
YOUNG, D. and Kearney, J.F.
SEQUENCE ANALYSIS AND ANTIGEN BINDING CHARACTERISTICS OF Ig SCID
Ig+ mice
Int. Immunol. 7 (5), 807-819 (1995)
JOURNAL 96053543
MEDLINE 7547707
PUBMED 7547707
REFERENCE 2 (bases 1 to 360)
AUTHORS Young, D.C.
TITLE Direct Submission
JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
Houston, TX 77030, USA
LOCATION/QUALIFIERS
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BASE COUNT 82 a 99 c 87 g 92 t
ORIGIN

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Query Match 82.5%; Score 299.6; DB 10; Length 360;
Best Local Similarity 91.2%; Pred. No. 5.6e-86;
Matches 330; Conservative 0; Mismatches 29; Indels 3; Gaps 1;

QY 1 CAGGTACTCTGAAGAGTCTGGCCCTGGGATATTGCAGCCCTCCAGACCCCTCAGTCTG 60
DB 1 CAGGTACTCTGAAGAGTCTGGCCCTGGGATATTGCAGTCTCCAGACCCCTCAGTCTG 60
QY 61 ACTTGTTCTTTCTCTGGGTTTTCACCTGAGCATTCTGGTATGGTGTGAGCTGGATTCTG 120
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DB 121 CAGCCTTCAGAAAGGCTCGAGTGGCTGGACACATTACTGGGATGATGACAGCGC 180
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QY 241 TTCCTCAAGATCACCAGTGTGACATCTGAGATATGCGGATCTGCTGCTCGAAGG 300
DB 241 TTCCTCAGGATCACCAGTGTGACATCTGAGATATGCGGATCTGCTGCTCGAAGG 300
QY 301 GTCTCTTAAGTCCCTATGATGAGTCTGAGTCTGAGGTCAGGAGACCTCAGTCAACCTCTCC 360
DB 301 G---CTCTAGGTAGTACCTACTTTGACTCTGCGGCGCAAGGACCACTCTCAGTCTCC 357
QY 361 TC 362
DB 358 TC 359

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RESULT 14
E07990
LOCUS DNA encoding inhibitor of binding IL-6 to its receptor.
DEFINITION E07990
ACCESSION E07990
VERSION E07990.1 GI:2176121
KEYWORDS JP 1994237772-A/1.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 738)
AUTHORS Shimamura, T., Nakazawa, H. and Hamuro, J.
TITLE IMMUNOSUPPRESSANT
JOURNAL Patent: JP 1994237772-A 1 30-AUG-1994;
AJINOMOTO CO INC
COMMENT OS Unknown
PN JP 1994237772-A/1
PD 30-AUG-1994
PF 17-FEB-1993 JP 1993028173
PI SHIMAMURA TOSHIKI, NAKAZAWA HARUMI, HAMURO JUNJI PC
C12N15/12, A61K37/02, A61K37/02, C12N15/70, C12P21/02; CC
strandedness: Double;
CC topology: Linear;

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EH Key Location/Qualifiers

EH source 1..738
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FT /cell_type='hybridoma'
FT /clone='HH61-10'
FT mat_peptide 1..738
FT /product='inhibitor of binding og IL-6 to its
FT receptor'

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source Location/Qualifiers
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BASE COUNT 187 a 189 c 180 g 182 t
ORIGIN

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Best Local Similarity 90.1%; Pred. No. 7.6e-86;
Matches 335; Conservative 0; Mismatches 28; Indels 9; Gaps 1;

QY 1 CAGGTTACTCTGAAAGAGTCTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCAGTCTG 60
DB 367 CAGGTCAACTCGAGGAGTCTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCAGTCTG 426
QY 61 ACTTGTTCTTCTCTGGGTTTCTACTGAGCACTTCTGGTATGGGTGTGAGCTGGATTGGA 120
DB 427 ACTTGTTCTTCTCTGGGTTTCTACTGAGCACTTCTGGTATGGGTGTGAGCTGGATTG 486
QY 121 CAGCCTTCAGGAAGGGTCTGGAGTGGCTGGGACACATTTACTGGGATGATGACAGGC 180
DB 487 CAGCCTTCAGGAAGGGTCTGGAGTGGCTGGGACACATTTACTGGGATGATGACAGGC 180
QY 181 TATAACCCATCCCTGAAGAGCGGCTTACAATCTCAAGGATACCTCCAGCAACCCAGGTA 240
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QY 241 TTCTCAAGATCAGAGTGGGACACTCGAGATCTGCCACATCTACTGTGCTCGAAG- 299
DB 607 TTCTCAAGATCAGAGTGGGACACTCGAGATCTGCCACATCTACTGTGCTCGAAG- 299
QY 300 -----GGTCTCTCTAACTGCTATGCTATGGACTACTGGGTCAAGGAACCTCAGTC 351
DB 667 AGTCTCTATGGTAATTGGGGGACTATGCTATGAGTACTGGGTCAAGGAACCTCAGTC 351
QY 352 ACCGTCTCTCA 363
DB 727 ACCGTCTCTCA 738

RESULT 15

I45910 LOCUS 738 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 6 from patent US 5639455.
ACCESSION I45910
VERSION I45910.1 GI:2469875
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 738)
AUTHORS Shimamura,T., Nakazawa,H. and Hamuro,J.
TITLE Immunosuppressant
JOURNAL Patent: US 5639455-A 6 17-JUN-1997;
FEATURES Location/Qualifiers
source 1..738
/organism='unknown'
BASE COUNT 187 a 189 c 180 g 182 t
ORIGIN

Query Match 82.4%; Score 299.2; DB 6; Length 738;
Best Local Similarity 90.1%; Pred. No. 7.6e-86;
Matches 335; Conservative 0; Mismatches 28; Indels 9; Gaps 1;

QY 1 CAGGTTACTCTGAAAGAGTCTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCAGTCTG 60
DB 367 CAGGTCAAACTCGAGGAGTCTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCAGTCTG 426
QY 61 ACTTGTTCTTCTCTGGGTTTCTACTGAGCACTTCTGGTATGGGTGTGAGCTGGATTGGA 120
DB 427 ACTTGTTCTTCTCTGGGTTTCTACTGAGCACTTCTGGTATGGGTGTGAGCTGGATTG 486
QY 121 CAGCCTTCAGGAAGGGTCTGGAGTGGCTGGGACACATTTACTGGGATGATGACAGGC 180
DB 487 CAGCCTTCAGGAAGGGTCTGGAGTGGCTGGGACACATTTACTGGGATGATGACAAAC 546
QY 181 TATAACCCATCCCTGAAGAGCGGCTTACAATCTCAAGGATACCTCCAGCAACCCAGGTA 240
DB 547 TATAACCCATCCCTGAAGAGCGGCTTACAATCTCAAGGATACCTCCAGCAACCCAGGTA 240
QY 241 TTCTCAAGATCAGAGTGGGACACTCGAGATCTGCCACATCTACTGTGCTCGAAG- 299
DB 607 TTCTCAAGATCAGAGTGGGACACTCGAGATCTGCCACATCTACTGTGCTCGAAG- 299
QY 300 -----GGTCTCTCTAACTGCTATGCTATGGACTACTGGGTCAAGGAACCTCAGTC 351
DB 667 AGTCTCTATGGTAATTGGGGGACTATGCTATGAGTACTGGGTCAAGGAACCTCAGTC 351
QY 352 ACCGTCTCTCA 363
DB 727 ACCGTCTCTCA 738

Search completed: January 14, 2004, 17:00:15
Job time : 1797.1 secs

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OM nucleic - nucleic search, using sw model

Run on: January 14, 2004, 14:23:59 ; Search time 186.476 Seconds
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Title: US-09-759-112a-5

Perfect score: 363

Sequence: 1 caggttactctgaagatgc.....cctcagtcacgcgtctctccta 363

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
1	363	100.0	363 24	AA148651 Murine Mab 1F7 hea
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3	313.4	86.3	483 16	AAQ83491 Mouse Mab 3B9 heav
4	313.4	86.3	483 20	AAQ85885 Heavy chain variab
5	313.4	86.3	483 20	AAQ79520 Heavy chain coding
6	311.8	85.9	423 16	AAQ83492 Chimeric antibody
7	311.8	85.9	423 20	AAQ85886 Heavy chain variab
8	311.8	85.9	423 20	AAQ79542 Chimeric 3B9 monoc

9	311.8	85.9	426	24	ABSS9429	Mouse 10D5 VH gene
10	303.6	83.6	366	15	AAQ68709	Humanised Mab H-ch
11	299.2	82.4	738	15	AAQ70612	IL-6 binding inhib
12	296.4	81.7	360	17	AAQ09300	Murine anti-Protei
13	296.4	81.7	417	17	AAQ09299	Murine heavy chain
14	291	80.2	418	16	AAQ75889	Mouse heavy chain
15	284.4	78.3	465	24	ABN84609	Anti-Streptococcus
16	283	78.0	1416	25	ABZ24639	Humanised 10D5 ant
17	283	78.0	3256	25	ABZ24641	Humanised 10D5 ant
18	282	77.7	1413	21	ABK11000	DNA encoding prote
19	269	74.1	354	21	AAK14500	DNA sequence #1 in
20	267	73.6	369	21	AAQ9646	Mouse antibody 13G
21	261.8	72.1	429	15	AAQ64166	Sequence of mouse
22	250.8	69.1	812	14	AAQ37056	Rat immunoglobulin
23	250.8	69.1	812	20	AAQ99479	KM50 Rat immunogl
24	250.8	69.1	812	21	AAK1000	Rat activated immu
25	249.2	68.7	812	15	AAQ45437	KM50 cell-derived
26	195.8	53.9	363	22	AAH42390	Nucleotide sequenc
27	191.4	52.7	423	14	AAQ45597	Sequence encoding
28	191.4	52.7	423	20	AAZ39427	Antibody B17X2 VH
29	191.4	52.7	423	20	AAZ23965	Human B17X2 antibo
30	190.6	52.5	423	20	AAQ79207	Anti-HIV-1 gp120 a
31	190.2	52.4	613	16	AAQ78943	Human immunoglobul
32	185.4	51.1	418	16	AAQ75916	Anti-human IL-6 ch
33	185.4	51.1	1607	22	AAQ66519	Human immune syste
34	184.6	50.9	444	18	AAQ80181	Monoclonal antibod
35	183.8	50.6	418	16	AAQ75917	Anti-human IL-6 ch
36	181.2	49.9	546	16	AAQ78964	Human immunoglobul
37	181	49.9	437	21	AAZ42289	Human 5' EST isola
38	180.4	49.7	1558	25	ABX12861	DNA encoding monoc
39	180.2	49.6	397	22	ABA08554	Human anti-HIV gpl
40	179.8	49.5	400	21	AAQ00033	Human secreted pro
41	172.6	47.5	630	16	AAQ78948	Human immunoglobul
42	171	47.1	423	16	AAQ83493	Humanized antibody
43	171	47.1	423	20	AAQ85887	Heavy chain variab
44	171	47.1	423	20	AAQ79516	Heavy chain coding
45	168.8	46.5	447	20	AAZ20406	IgG antibody 2.4.4

ALIGNMENTS

RESULT 1

AL48651
ID AAL48651 standard; DNA; 363 BP.

XX AAL48651;

XX DT 11-OCT-2002 (first entry)

XX DE Murine Mab 1F7 heavy chain coding sequence.

XX KW Mouse; 1F7; antibody; immune modulator; anti-HIV antibody; CDR;
KW complementarity determining region; framework-determining region;
KW FR; heavy chain; light chain; HIV infection; gene; ss.

XX OS Mus sp.

XX PN WO200255668-A2.

XX PD 18-JUL-2002.

XX PF 11-JAN-2002; 2002WO-US000927.

XX PR 11-JAN-2001; 2001US-0759112.

XX PA (IMMP-) IMMOPHERON INC.

XX PI Muller S, Kohler H;

XX XX WPI; 2002-590668/63.

XX PT New polynucleotide encoding a complementarity- or framework-determining

PT region of an anti-idiotypic antibody that binds to human or primate
PT anti- human immunodeficiency virus (HIV) antibodies, for use in
PT vaccines against HIV -
XX
XX Claim 10; Page 17; 27pp; English.
XX
XX The present invention relates to coding sequences of the murine 1F7
CC anti-idiotypic antibody complementarity-determining region (CDR) or
CC framework-determining region (FR). The antibody binds to human or primate
CC anti-human immunodeficiency virus (HIV) antibodies and can be used in the
CC treatment of HIV infection. The present sequence is the 1F7 heavy chain
CC coding sequence.
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XX Sequence 363 BP; 83 A; 100 C; 88 G; 92 T; 0 other;
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Query Match 100.0%; Score 363; DB 24; Length 363;
Best Local Similarity 100.0%; Pred. No. 7.7e-102;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGCGACCCCTCCAGACCCCTCAGTCTG 60
DB 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGCGACCCCTCCAGACCCCTCAGTCTG 60
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DB 61 ACTTGTTCTTCTCTGGGTTTTCACAGACCTTCTGGTATGGGTGAGCTGGATTGGA 120
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OY 181 TATAACCCATCCCTGAAGAGCGGCTTACATCTCCAGGATACCTCCAGCAACCCAGGTA 240
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OY 361 TCA 363
DB 361 TCA 363
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AAL48652
ID AAL48652 standard; DNA; 363 BP.
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XX AAL48652;
XX
XX 11-OCT-2002 (first entry)
XX
XX Murine Mab 1F7 heavy chain coding sequence.
XX
XX Mouse; 1F7; antibody; immune modulator; anti-HIV antibody; CDR;
XX complementarity determining region; framework-determining region;
XX FR; heavy chain; light chain; HIV infection; gene; ss.
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XX Mus sp.
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XX Key Location/Qualifiers
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XX WO200255668-A2.
XX
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PD 18-JUL-2002.
XX
XX 11-JAN-2002; 2002WO-US00927.
XX
XX 11-JAN-2001; 2001US-0759112.
XX
XX (IMMP-) IMPHERON INC.
XX
XX Muller S, Kohler H;
XX
XX WPI; 2002-590668/63.
XX
XX P-PSDB; AAC18528.
XX
XX New polynucleotide encoding a complementarity- or framework-determining
XX region of an anti-idiotypic antibody that binds to human or primate
XX anti- human immunodeficiency virus (HIV) antibodies, for use in
XX vaccines against HIV -
XX
XX Disclosure; Page 17-18; 27pp; English.
XX
XX The present invention relates to coding sequences of the murine 1F7
XX anti-idiotypic antibody complementarity-determining region (CDR) or
XX framework-determining region (FR). The antibody binds to human or primate
XX anti-human immunodeficiency virus (HIV) antibodies and can be used in the
XX treatment of HIV infection. The present sequence is the 1F7 heavy chain
XX coding sequence.
XX
XX Sequence 363 BP; 83 A; 100 C; 88 G; 92 T; 0 other;
SQ
Query Match 100.0%; Score 363; DB 24; Length 363;
Best Local Similarity 100.0%; Pred. No. 7.7e-102;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGCGACCCCTCCAGACCCCTCAGTCTG 60
DB 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGCGACCCCTCCAGACCCCTCAGTCTG 60
OY 61 ACTTGTTCTTCTCTGGGTTTTCACAGACCTTCTGGTATGGGTGAGCTGGATTGGA 120
DB 61 ACTTGTTCTTCTCTGGGTTTTCACAGACCTTCTGGTATGGGTGAGCTGGATTGGA 120
OY 121 CAGCCCTTCAGGAAGGCTCTGGAGTGGCTGGGCACACATTTACTGGGATGATGACAAGCGC 180
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OY 361 TCA 363
DB 361 TCA 363
RESULT 3
AAQ83491
ID AAQ83491 standard; cDNA; 483 BP.
XX
XX AAQ83491;
XX
XX 25-MAR-2003 (updated)
XX
XX 20-SEP-1995 (first entry)
XX
XX Mouse Mab 3B9 heavy chain.
XX
XX

KW Chimeric antibody; humanized antibody; antibody engineering;
XX monoclonal antibody; Mab; interleukin-4; IL-4; allergy; ds.
OS Mus sp.

XX Key Location/Qualifiers
FH CDS 64..483
FT FT /*tag= a
FT sig_peptide 64..120
FT FT /*tag= b
FT mat_peptide 121..483
FT FT /*tag= c

XX MO9507301-A1.

XX 16-MAR-1995.

XX 07-SEP-1994; 94WO-US10308.

XX 07-SEP-1993; 93US-0117366.

XX 14-OCT-1993; 93US-0136783.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Gross MS, Holmes SD, Sylvester DR;

XX WPI; 1995-123387/16.

XX P-PSDB; AAR70190.

XX Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated and IgE-mediated allergic conditions

XX Disclosure; Fig.2; 97pp; English.

XX Spleen cells from mice immunized with human IL-4 were used to prepare hybridomas, which were screened for anti-IL-4 Mab secretion. Only clone 3B9 was positive. CDNA clones of the 3B9 light and heavy chains were cloned into pGEN7f+ and transformed into E. coli DH5-alpha. The clones were sequenced (AAQ83490-91), and used for antibody engineering.

XX (Updated on 25-MAR-2003 to correct FN field.)

XX Sequence 483 BP; 108 A; 130 C; 124 G; 121 T; 0 other;

XX Query Match 86.3%; Score 313.4; DB 16; Length 483;

XX Best Local Similarity 91.5%; Pred. No. 1.6e-86;

XX Matches 332; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1 CAGGTTACTCTGAAGAGCTGGCCCTGGGATTTGCAGCCCTCCAGACCTCAGTCTG 60

DB 121 CAGGTTACTCTGAAGAGCTGGCCCTGGGATTTGCAGCCCTCCAGACCTCAGTCTG 180

QY 61 ACTTGTCTTCTCTCGGTTTTCACATGACACTCTGGTATGGGTGAGCTGGATTGGA 120

DB 181 ACTTGTCTTCTCTCGGTTTTCACATGACACTCTGGTATGGGTGAGCTGGATTGGA 240

QY 121 CAGCCTTCAGGAAAGGCTCTGAGTGGCTGGGCACACATTTACTTGGATGATCAAGCGC 180

DB 241 CAGCCTTCAGGAAAGGCTCTGAGTGGCTGGGCACACATTTACTTGGATGATCAAGCGC 300

QY 181 TATAACCCATCCTGAGAGCGGCTTACAATCTCCAGGATACCTCCAGCAACAGGTA 240

DB 301 TATAACCCATCCTGAGAGCGGCTTACAATCTCCAGGATACCTCCAGCAACAGGTA 360

QY 241 TTCTCAAGATCACCAAGTGTGGACACTCGAGATACCTGATCTGTGCTCGAAGG 300

DB 361 TTCTCAAGATCACCAAGTGTGGACACTCGAGATACCTGATCTGTGCTCGAAGG 420

QY 301 GTCTCTCTACTGCTTATGCTATGACTACTGGGTCAAGGAACCTCAGTACCGTCTCC 360

DB 421 GAGACTGTGTTCTACTGGTACTTCGATGTCTGGGGCGCAGGACCGGTACCGTCTCC 480

QY 361 TCA 363
DB 481 TCA 483

RESULT 4

AA85885

ID AAX85885 standard; CDNA; 483 BP.

XX AC AAX85885;

XX 13-SEP-1999 (first entry)

XX Heavy chain variable region cDNA of murine IL-4 antibody 3B9.

XX Heavy chain variable region; interleukin-4; IL-4; antibody 3B9;

XX chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;

XX Immunoglobulin E-mediated allergic reaction; allergic rhinitis;

XX conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;

XX rheumatoid arthritis; host-versus-graft disease; renal disease;

XX allergy; ds.

XX Mus sp.

XX US5928904-A.

XX 27-JUL-1999.

XX 07-JUN-1995; 95US-0483632.

XX 07-JUN-1995; 95US-0483632.

XX 07-SEP-1993; 93US-0117366.

XX 14-OCT-1993; 93US-0136783.

XX 07-SEP-1994; 94WO-US10308.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Gross MS, Holmes SD, Sylvester DR;

XX WPI; 1999-429500/36.

XX P-PSDB; AAY23768.

XX New DNA molecules encoding recombinant antibodies useful for treating IL4-mediated conditions

XX Claim 3; Fig 2; 50pp; English.

XX The present sequence encodes the heavy chain variable region of murine interleukin-4 (IL-4) antibody 3B9. The sequences are used in the production of chimeric and humanised IL-4 monoclonal antibodies. The antibodies of the invention are used in therapeutic and pharmaceutical compositions for treating IL-4 mediated and immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis, conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock, rheumatoid arthritis, host-versus-graft disease and renal disease. They are also useful in the diagnosis of an allergy or condition associated with excess IL-4 production through the measurement e.g. by ELISA of circulating endogenous IL-4 levels in humans.

XX Sequence 483 BP; 108 A; 130 C; 124 G; 121 T; 0 other;

XX Query Match 86.3%; Score 313.4; DB 20; Length 483;

XX Best Local Similarity 91.5%; Pred. No. 1.6e-86;

XX Matches 332; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1 CAGGTTACTCTGAAGAGCTGGCCCTGGGATTTGCAGCCCTCCAGACCTCAGTCTG 60

DB 121 CAGGTTACTCTGAAGAGCTGGCCCTGGGATTTGCAGCCCTCCAGACCTCAGTCTG 180

QY 61 ACTTGTCTTCTCTCGGTTTTCACATGACACTCTGGTATGGGTGAGCTGGATTGGA 120

DB 181 ACTTGTCTTCTCTCGGTTTTCACATGACACTCTGGTATGGGTGAGCTGGATTGGA 240

QY 121 CAGCCTTCAGGAAAGGCTCTGAGTGGCTGGGCACACATTTACTTGGATGATCAAGCGC 180

DB 241 CAGCCTTCAGGAAAGGCTCTGAGTGGCTGGGCACACATTTACTTGGATGATCAAGCGC 300

QY 181 TATAACCCATCCTGAGAGCGGCTTACAATCTCCAGGATACCTCCAGCAACAGGTA 240

DB 301 TATAACCCATCCTGAGAGCGGCTTACAATCTCCAGGATACCTCCAGCAACAGGTA 360

QY 241 TTCTCAAGATCACCAAGTGTGGACACTCGAGATACCTGATCTGTGCTCGAAGG 300

DB 361 TTCTCAAGATCACCAAGTGTGGACACTCGAGATACCTGATCTGTGCTCGAAGG 420

QY 301 GTCTCTCTACTGCTTATGCTATGACTACTGGGTCAAGGAACCTCAGTACCGTCTCC 360

DB 421 GAGACTGTGTTCTACTGGTACTTCGATGTCTGGGGCGCAGGACCGGTACCGTCTCC 480


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DR WPI; 1995-123387/16.
XX P-PSDB; AAR70191.
XX
XX Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
PT from high affinity mAbs - useful in treatment of IL-4-mediated
PT and IgE-mediated allergic conditions
XX
XX Disclosure; Fig.3; 97pp; English.
XX
XX A human/mouse chimeric antibody heavy chain variable region was
CC constructed (given in AAR70191) that contained the mouse anti-human
CC IL-4 MAb 3B9 variable region including 3 CDRs (AAR70198-200) and a
CC human antibody signal peptide (AAR70193). The construct was used
CC for humanized antibody production.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 423 BP; 87 A; 115 C; 110 G; 111 T; 0 other;
XX
Query Match      85.9%; Score 311.8; DB 16; Length 423;
Best Local Similarity 91.2%; Pred. No. 4.8e-86;
Matches 331; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 1 CAGGTTACTCTGAAAGAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCCCTCAGTCTG 60
DB 61 CAGGTTACCTCTGAAAGAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCCCTCAGTCTG 120
QY 61 ACTTGTTCTTCTCTGGGTTTTCACCTGAGCAGCTCTCTGGTATGGGTGAGTTCGA 120
DB 121 ACTTGTTCTTCTCTGGGTTTTCACCTGAGCAGCTCTCTGGTATGGGTGAGTTCGT 180
QY 121 CAGCCTTCAGGAAGGTCCTGGAGTGGCTGGCCACATTTACTGGGATGATGACAGCC 180
DB 181 CAGCCTTCAGGAAGGTCCTGGAGTGGCTGGCCACATTTACTGGGATGATGACAGCC 240
QY 181 TATAACCCATCCCTGAAAGAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCCAGGTA 240
DB 241 TATAACCCATCCCTGAAAGAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCCAGGTA 300
QY 241 TTCTCTAAGATCACCAGTGTGGACACTGCGAGTACTGCGGCTCAAGAACCTCAGTCCCGTCC 300
DB 301 TTCTCTAAGATCACCAGTGTGGACACTGCGAGTACTGCGGCTCAAGAACCTCAGTCCCGTCC 360
QY 301 GTCTCTTCTAACTGGCTATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCCCGTCC 360
DB 361 GAGACTGTGTTCTACTGGTACTTCGATGCTGGGGCGCAGGACCCAGGTCACCGTCTCC 420
QY 361 TCA 363
DB 421 TCA 423
XX
RESULT 7
AAK85886
ID AAK85886 standard; cDNA; 423 BP.
AC AAK85886;
XX
XX 13-SEP-1999 (first entry)
XX
XX Heavy chain variable region cDNA of murine/human chimeric antibody 3B9.
XX
XX Heavy chain variable region; interleukin-4; IL-4; antibody 3B9;
XX chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;
XX Immunoglobulin B-mediated allergic reaction; allergic rhinitis;
XX conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
XX rheumatoid arthritis; host-versus-graft disease; renal disease;
XX allergy; ds.
XX
XX Chimeric - Mus sp.
XX Chimeric - Homo sapiens.
XX
XX US5928904-A.

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PD 27-JUL-1999.
XX
XX 07-JUN-1995; 95US-0483632.
XX
XX 07-JUN-1995; 95US-0483632.
PR 07-SEP-1993; 93US-0117366.
PR 14-OCT-1993; 93US-0136783.
PR 07-SEP-1994; 94WO-US10308.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Gross MS, Holmes SD, Sylvester DR;
XX
XX WPI; 1999-429500/36.
XX P-PSDB; AAY23769.
XX
XX New DNA molecules encoding recombinant antibodies useful for
PT treating IL4-mediated conditions
PT
XX
XX Example 3; Fig 3; 50pp; English.
XX
XX The present sequence encodes the heavy chain variable region of
CC murine/human interleukin-4 (IL-4) chimeric antibody 3B9. The
CC specification describes chimeric and humanised IL-4 monoclonal
CC antibodies. The antibodies of the invention are used in therapeutic
CC and pharmaceutical compositions for treating IL-4 mediated and
CC immunoglobulin B-mediated allergic reactions e.g. allergic rhinitis,
CC conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock,
CC rheumatoid arthritis, host-versus-graft disease and renal disease.
CC They are also useful in the diagnosis of an allergy or condition
CC associated with excess IL-4 production through the measurement e.g. by
CC ELISA of circulating endogenous IL-4 levels in humans.
XX
XX Sequence 423 BP; 87 A; 115 C; 110 G; 111 T; 0 other;
XX
Query Match      85.9%; Score 311.8; DB 20; Length 423;
Best Local Similarity 91.2%; Pred. No. 4.8e-86;
Matches 331; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 1 CAGGTTACTCTGAAAGAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCCCTCAGTCTG 60
DB 61 CAGGTTACCTCTGAAAGAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCCCTCAGTCTG 120
QY 61 ACTTGTTCTTCTCTGGGTTTTCACCTGAGCAGCTCTCTGGTATGGGTGAGTTCGA 120
DB 121 ACTTGTTCTTCTCTGGGTTTTCACCTGAGCAGCTCTCTGGTATGGGTGAGTTCGT 180
QY 121 CAGCCTTCAGGAAGGTCCTGGAGTGGCTGGCCACATTTACTGGGATGATGACAGCC 180
DB 181 CAGCCTTCAGGAAGGTCCTGGAGTGGCTGGCCACATTTACTGGGATGATGACAGCC 240
QY 181 TATAACCCATCCCTGAAAGAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCCAGGTA 240
DB 241 TATAACCCATCCCTGAAAGAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCCAGGTA 300
QY 241 TTCTCTAAGATCACCAGTGTGGACACTGCGAGTACTGCGGCTCAAGAACCTCAGTCCCGTCC 300
DB 301 TTCTCTAAGATCACCAGTGTGGACACTGCGAGTACTGCGGCTCAAGAACCTCAGTCCCGTCC 360
QY 301 GTCTCTTCTAACTGGCTATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCCCGTCC 360
DB 361 GAGACTGTGTTCTACTGGTACTTCGATGCTGGGGCGCAGGACCCAGGTCACCGTCTCC 420
QY 361 TCA 363
DB 421 TCA 423
XX
RESULT 8
AAK79542
ID AAK79542 standard; cDNA; 423 BP.
XX

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QY 121 CAGCCTTCAGGAAGGGTCTGGAGTGGCTGGCACACATTACTGGGATGATGACAAAGCGC 180
Db 178 CAGCCTTCAGGAAGGGTCTGGAGTGGCTGGCACACATTACTGGGATGATGACAAAGCGC 237
QY 181 TATAAACCATTCCCTGAAGAGCGCGCTTACAAATCTCCAAGGATACCTCCAGCAACACAGGTA 240
Db 238 TATAAACCATTCCCTGAAGAGCGCGCTCACAATCTCCAAGGATACCTCCAGCAACACAGGTA 297
QY 241 TTCTCTCAAGATCAGCAGTGTGGACATCTGAGATGACTGCCACATCTACTGTGCTCGAAGG 300
Db 298 TTCTCTCAAGATCAGCAGTGTGGACATCTGAGATGACTGCCACATCTACTGTGCTCGAAGG 357
QY 301 GTC-----TCTCTAAGTCTGCTATGCTATGCTACTTGGGGTCAAGGAACTCAGTCACC 354
Db 358 CCATTAATCTCGGTACTAGTCTGATGCTATGCTACTTGGGGTCAAGGAACTCAGTCACC 417
QY 355 GTCTCTCA 363
Db 418 GTCTCTCA 426
RESULT 10
AAQ68709
ID AAQ68709 standard; cDNA to mRNA; 366 BP.
XX AC AAQ68709;
XX XX
DT 08-FEB-1995 (first entry)
DE Humanised MAb H-chain coding sequence.
XX Human; mouse; murine; heavy; light; chain; monoclonal; antibody;
KW complementarity determining region; CDR; IgG; kappa; IIIB; IIMN; ds.
XX Chimeric - Mus musculus.
OS Chimeric - Homo sapiens.
XX JF06141885-A.
PN 24-MAY-1994.
XX 05-NOV-1992; 92JP-0322476.
XX 05-NOV-1992; 92JP-0322476.
PR (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX WPI; 1994-205040/25.
XX P-PSDB; AAR54101.
XX Recombinant anti-HIV monoclonal antibody - capable of
PT neutralising strains which can not be neutralised by anti-IIIB
PT and IIMN antibodies
XX Disclosure; Page 13; 23pp; Japanese.
XX The sequences given in AAQ68709-10 encode the heavy and light chains
CC respectively of the humanised monoclonal antibody (MAb) of the
CC invention. The antibody has the ability to neutralise human
CC immunodeficiency virus. The antibody is classified as IgG kappa and
CC has the sequence RIGPKR or RVGPKR in the principal neutralising
CC domain. The antibody may be used to neutralise the clinically
CC separate strains which cannot be neutralised by the neutralising
CC antibodies against IIIB and IIMN strains.
XX SQ Sequence 366 BP; 85 A; 98 C; 84 G; 99 T; 0 other;
Query Match 83.6%; Score 303.6; DB 15; Length 366;
Best Local Similarity 91.3%; Pred. No. 1.5e-83;
Matches 334; Conservative 0; Mismatches 29; Indels 3; Gaps 1;
QY 1 CAGGTACTCTGAAGAGTCTGGCCCTGGTATATTCAGCCCTCCACAGACCTCAGTCTG 60

Db 1 CAGGTACTCTGAAGAGTCTGGCCCTGGTATATTCAGCCCTCCACAGACCTCAGTCTG 60
QY 61 ACTTGTCTCTTCTCTGGGTTTTCATCGAGCACATTTCTGGTATGGGTGTGAGCTGGATTGGA 120
Db 61 ACTTGTCTCTTCTCTGGGTTTTCATCGAGCACATTTCTGGTATGGGTGTGAGCTGGATTGCGT 120
QY 121 CAGCCTTCAGGAAGGGTCTGGAGTGGCTGGCACACATTTACTGGGATGATGACAAAGCGC 180
Db 121 CAGCCTTCAGGAAGGGTCTGGAGTGGCTGGCACACATTTATTGGGATGATGACAAAGCAC 180
QY 181 TATAAACCATTCCCTGAAGAGCGCGCTTACAAATCTCCAAGGATACCTCCAGCAACACAGGTA 240
Db 181 TATAAACCATTCCCTGAAGAGCGCGCTCACAATCTCCAAGGATACCTCCACAAATCAGGTA 240
QY 241 TTCTCTCAAGATCAGCAGTGTGGACATCTGAGATGACTGCCACATCTACTGTGCTCGAAGG 300
Db 241 TTCTCTCAAGATCAGCAGTGTGGACATCTGAGATGACTGCCACATCTACTGTGCTCGAAGG 300
QY 301 G---TCTCTCTAAGTCTGGCTATGCTATGAGTCTACTGGGGTCAAGGAACTCAGTCACCGTC 357
Db 301 GTCTCTATGCTTAAGTCTGGATTTTATGACCACTGGGGTCAAGGAACTCAGTCACCGTC 360
QY 358 TCCTCA 363
Db 361 TCCTCA 366
RESULT 11
AAQ70612
ID AAQ70612 standard; DNA; 738 BP.
XX AC AAQ70612;
XX 25-MAR-2003 (updated)
DT 28-APR-1995 (first entry)
XX IL-6 binding inhibitor DNA.
DE Human interleukin-6 binding inhibitor; IL-6; rheumatoid arthritis;
KW septic shock; multiple myeloma; ss.
XX Homo sapiens.
XX EP617126-A2.
PN 28-SEP-1994.
XX 16-FEB-1994; 94EP-0102346.
XX 17-FEB-1993; 93JP-0028173.
XX (AJIN) AJINOMOTO KK.
XX Hamuro J, Nakazawa H, Shimamura T;
PI WPI; 1994-295777/37.
DR P-PSDB; AAR58612.
XX Polypeptide inhibiting binding of human interleukin-6 (IL-6) to
PT its receptor - useful for treating autoimmune disease induced
PT or aggravated by IL-6
XX Claim 9; Page 19; 26pp; English.
XX AAQ70612 codes for human interleukin-6 binding inhibitor, the
CC polypeptide described in AAR58612. This polypeptide inhibits the
CC binding of human IL-6 to its receptor, and can therefore be
CC useful in the treatment of a variety of autoimmune diseases;
CC specifically in the treatment of rheumatoid arthritis, septic
CC shock due to bacterial infection and multiple myeloma.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX

SQ Sequence 738 BP; 187 A; 189 C; 180 G; 182 T; 0 other;

Query Match 82.4%; Score 299.2; DB 15; Length 738;
Best Local Similarity 90.1%; Pred. No. 4.4e-82;
Matches 335; Conservative 0; Mismatches 28; Indels 9; Gaps 1;

QY 1 CAGGTACTCTGAAGAGTCTGGCCCTGGGATATTGCAGCCCTCCAGACCCCTCAGTCTG 60
DB 367 CAGGTCAAACTCGAGAGTCTGGCCCTGGGATATTGCAGCCCTCCAGACCCCTCAGTCTG 426

QY 61 ACTTGTTCTTTCTCTGGTTTCTACAGACCTCTCTGGTATGGGTGAGCTGGATTGGA 120
DB 427 ACTTGTTCTTTCTCTGGTTTCTACAGACCTCTCTGGTATGGGTGAGCTGGATTGGA 486

QY 121 CAGCCCTCAGGAAGAGTCTGGAGTGGCTGGCACACATTTACTGGGATGATGACAAAGCGC 180
DB 487 CAGCCCTCAGGAAGAGTCTGGAGTGGCTGGCACACATTTATTGGATGATGACAAACAC 546

QY 181 TATAACCCATCCCTGAAGAGCCGGTTTCAATCTCCAGGATACCTCCAGCAACAGGTA 240
DB 547 TATAACCCATCCCTGAAGAGCCGGTTTCAATCTCCAGGATACCTCCAGCAACAGGTA 606

QY 241 TTCTCTCAAGATCACCAGTGTGGACACTCGAGATACCTGCCACATCTACTGTCTGGAAG- 299
DB 607 TTCTCTCAAGATCACCAGTGTGGACACTCGAGATACCTGCCACATCTACTGTCTGGAAG 666

QY 300 -----GGTCTCTCTAACTGGCTATGCTATGGACTACTGGGGTCAAGGAACCTCAGTC 351
DB 667 AGTCTCTATGTAATTTGGGGGACTATGCTATGGACTACTGGGGTCAAGGAACCTCAGTC 726

QY 352 ACCGTCCTCTCA 363
DB 727 ACCGTCCTCTCA 738

RESULT 12
AAT09300
ID AAT09300 standard; DNA; 360 BP.
XX
AC AAT09300;
XX
XX
DT 25-JUL-1996 (first entry)
XX
DE Murine anti-Protein C Mab HPC-4 VH gamma mature protein coding region.
XX
KW Epitope; activation; heavy chain; protein C; vitamin K; plasma protein;
KW zymogen; cleavage; mouse; humanised antibody; variable region;
KW light chain; inhibition; anticoagulant; coagulation; tumour; ss.
XX
OS Mus musculus.
XX
PN W09534652-A1.
XX
PD 21-DEC-1995.
XX
PF 09-JUN-1995; 95WO-US07372.
XX
PR 10-JUN-1994; 94US-0259321.
XX
XX (OKLA-) OKLAHOMA MED RES FOUND.
PA
PI Esmon CT, Rezaie A;
XX
XX WPI; 1996-049681/05.
XX P-PSDB; AAR88109.
XX
XX Calcium-binding monoclonal antibody immunoreactive with Protein C -
FT inhibits Protein C anticoagulant activation by
FT thrombin-thrombomodulin, e.g. for treating tumours
XX
XX Claim 4; Page 30; 41pp; English.
PS
XX This is the nucleotide sequence encoding the mature protein from the

CC murine anti-protein C monoclonal antibody HPC-4 heavy chain variable
CC region (VH gamma). HPC-4 recognises the activation peptide region
CC (AAR8106) of the heavy chain of protein C, a vitamin K-dependent plasma
CC protein zymogen. Protein C is activated to activated protein C (APC)
CC by cleavage between the Arg-leu amino acid contained within the
CC activation peptide sequence. HPC-4 prevents protein C activation to
CC APC by binding to this region. The DNA sequences encoding the variable
CC regions of the heavy and light chains of the antibody (AAT09299-302)
CC were used to construct humanised antibodies using the PCR primers
CC AAT09303-9. The humanised antibodies are useful as inhibitors of
CC coagulation and can be used for the treatment of tumours by inhibiting
CC the anticoagulant activity of APC by preventing conversion of protein C
CC to APC.
XX

SQ Sequence 360 BP; 82 A; 91 C; 95 G; 92 T; 0 other;

Query Match 81.7%; Score 296.4; DB 17; Length 360;
Best Local Similarity 90.6%; Pred. No. 2.5e-81;
Matches 328; Conservative 0; Mismatches 31; Indels 3; Gaps 1;

QY 1 CAGGTACTCTGAAGAGTCTGGCCCTGGGATATTGCAGCCCTCCAGACCCCTCAGTCTG 60
DB 1 CAGGTACTCTGAAGAGTCTGGCCCTGGGATATTGCAGCCCTCCAGACCCCTCAGTCTG 60

QY 61 ACTTGTTCTTTCTCTGGTTTCTACAGACCTCTCTGGTATGGGTGAGCTGGATTGGA 120
DB 61 ACTTGTTCTTTCTCTGGTTTCTACAGACCTCTCTGGTATGGGTGAGCTGGATTGGA 120

QY 121 CAGCCCTCAGGAAGAGTCTGGAGTGGCTGGCACACATTTACTGGGATGATGACAAAGCGC 180
DB 121 CAGCCCTCAGGAAGAGTCTGGAGTGGCTGGCACACATTTGGTGGGATGATGACAAAGCGC 180

QY 181 TATAACCCATCCCTGAAGAGCCGGTTTCAATCTCCAGGATACCTCCAGCAACAGGTA 240
DB 181 TATAACCCATCCCTGAAGAGCCGGTTTCAATCTCCAGGATACCTCCAGCAACAGGTA 240

QY 241 TTCTCTCAAGATCACCAGTGTGGACACTCGAGATACCTGCCACATCTACTGTCTGGAAG 300
DB 241 TTCTCTCAAGATCACCAGTGTGGACACTCGAGATACCTGCCACATCTACTGTCTGGAAG 300

QY 301 GTCTCTCTAACTGGCTATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCC 360
DB 301 ATGGAT---GATTACGACGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCC 357

QY 361 TC 362
DB 358 TC 359

RESULT 13
AAT09299
ID AAT09299 standard; DNA; 417 BP.
XX
AC AAT09299;
XX
DT 25-JUL-1996 (first entry)
XX
DE Murine anti-Protein C Mab HPC-4 VH gamma coding region.
XX
KW Epitope; activation; heavy chain; protein C; vitamin K; plasma protein;
KW zymogen; cleavage; mouse; humanised antibody; variable region;
KW light chain; inhibition; anticoagulant; coagulation; tumour; ss.
XX
OS Mus musculus.
XX
XX Key Location/Qualifiers
FH sig_peptide 1..57
FT /*tag= a
FT mat_peptide 58..417
FT /*tag= b
XX
XX W09534652-A1.
PN
XX

PD 21-DEC-1995.
XX 09-JUN-1995; 95WO-US07372.
XX 10-JUN-1994; 94US-0259321.
XX (OKLA-) OKLAHOMA MED RES FOUND.
PA Esmon CT, Rezaie A;
XX WPI; 1996-049681/05.
DR P-PSDB; AAR88107.
XX Calcium-binding monoclonal antibody immunoreactive with Protein C -
PT Inhibits Protein C anticoagulant activation by
PT thrombin-thrombomodulin, e.g. for treating tumours
XX Claim 4; Page 29-30; 4lpp; English.
XX This is the nucleotide sequence encoding the heavy chain variable region
CC from the murine anti-protein C monoclonal antibody HPC-4 which
CC recognises the activation peptide region (AAR88106) of the heavy chain of
CC protein C, a vitamin K-dependent plasma protein zymogen. Protein C is
CC converted to activated protein C (APC) by cleavage between the Arg-Leu
CC amino acid contained within the activation peptide sequence. HPC-4
CC prevents protein C activation to APC by binding to this region. The DNA
CC sequences encoding the variable regions of the heavy and light chains of
CC the antibody (AAR09299-302) were used to construct humanised antibodies
CC using the PCR primers AAR09303-9. The humanised antibodies are useful as
CC inhibitors of coagulation and can be used for the treatment of tumours by
CC inhibiting the anticoagulant activity of APC by preventing conversion of
CC protein C to APC.
XX
SQ Sequence 417 BP; 89 A; 108 C; 106 G; 114 T; 0 other;

Query Match 81.7%; Score 296.4; DB 17; Length 417;
Best Local Similarity 90.6%; Pred.No. 2.6e-81;
Matches 328; Conservative 0; Mismatches 31; Indels 3; Gaps 1;

QY 1 CAGGTACTCTGAAAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGTCTG 60
Db 58 CAGGTACTCTGAAAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGTCTG 117

QY 61 ACTTGTTCTTCTCTGGTTTTCACGTAGCAGCACTCTGGTATGGGTGTGAGCTGGATTGCA 120
Db 118 ACTTGTTCTTCTCTGGTTTTCACGTAGCAGCACTCTGGTATGGGTGTGAGCTGGATTGCT 177

QY 121 CAGCCTTCAGGAAAGGCTCTGGAGTGGCTGGCACACATTTACTGGGATGATGACAGCGC 180
Db 178 CAGCCTTCAGGAAAGGCTCTGGAGTGGCTGGCACACATTTGGTGGATGATGACAGCGC 237

QY 181 TATAACCCATCCTGAGAGCCGGCTTACATCTCCAGGATACCTCCAGCAACAGGTA 240
Db 238 TATAACCCATCCTGAGAGCCGGCTTACATCTCCAGGATACCTCCAGCAACAGGTA 297

QY 241 TTCTCTAAGTATCACCAGTGTGGACACTCCAGATCTGCCATPACTACTGTGTCGAAGG 300
Db 298 TTCTCTAAGTATCACCAGTGTGGACACTCCAGATCTGCCATPACTACTGTGTCGAAGG 357

QY 301 GTCTCTTAAGTATCACCAGTGTGGACACTCCAGATCTGCCATPACTACTGTGTCGAAGG 360
Db 358 ATGGAT---GATTACGACGCTATGGACTACTGGGGTCAAGGAACCTCAGTACCGGTCC 414

QY 361 TC 362
Db 415 TC 416

RESULT 14
ID AAQ75889
XX AAQ75889 standard; cDNA; 418 BP.
AC AAQ75889;

XX 25-MAR-2003 (updated)
DT 21-AUG-1995 (first entry)
XX Mouse heavy chain variable region in plasmid pUC-SK2-Vh.
XX Primer; PCR; amplif; kappa; light chain; variable region; mouse; human;
KW interleukin; antibody; hybridoma; CDR; framework; constant region;
XX heavy chain; disorder; antigenicity; ds.
OS Synthetic.
FH Key Location/Qualifiers
CDS 1..417 /*tag= a
FT /product= mouse heavy chain variable region
FT sig_peptide /*tag= b
FT mat_peptide /*tag= c
XX WO9428159-A1.
XX 08-DEC-1994.
XX 30-MAY-1994; 94WO-JP00859.
XX 31-MAY-1993; 93JP-0129787.
XX (CHUS) CHUGAI SEIYAKU KK.
PA (CHUS) CHUGAI PHARM CO LTD.
XX Hirata Y, Sato K, Tsuchiya M;
XX WPI; 1995-022828/03.
DR P-PSDB; AAR67655.
XX Antibody against IL-6 - useful for the therapy and treatment of
PT IL-6 related disorders.
PS Claim 10; Page 49; 82pp; Japanese.
XX The sequence of the gene encoding the heavy chain variable region of
CC the mouse anti-human interleukin-6 (IL-6) antibody. The fragment was
CC amplified by primers (AAQ75876-87) from cDNA derived from mRNA from
CC mouse SK2 hybridoma cells. The fragment was cloned into plasmid pUC19
CC to produce plasmid pUC-SK2-Vh. The inserted fragment is used to
CC generate constructs (see AAQ75914-7) encoding fragments of an antibody to
CC the human IL-6 comprising (a) a light chain with (i) a variable region
CC containing 3 complementarity determining regions (CDR) (AAR77201-3)
CC inserted into several framework regions (FR) (AAR77204-7) and (ii) a human
CC light chain constant region and (b) a heavy chain with (i) a variable
CC region containing 3 CDR (AAR77212-4) inserted into an FR (AAR77215-8) and
CC (ii) a human light chain constant region. The FR of the light chain may
CC be mouse derived (AAQ75888) or from the human antibody RE1. The heavy
CC chain FR may also be mouse derived (AAQ75889) or from the human antibody
CC DAW. The antibodies can be used in the treatment of IL-6 related
CC disorders. The antibodies are useful as they have low antigenicity due to
CC the use of human derived sequences and low antigenicity mouse derived
CC sequences.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX Sequence 418 BP; 96 A; 113 C; 99 G; 110 T; 0 other;

Query Match 80.2%; Score 291; DB 16; Length 418;
Best Local Similarity 89.5%; Pred.No. 1.2e-79;
Matches 325; Conservative 0; Mismatches 35; Indels 3; Gaps 1;

QY 1 CAGGTACTCTGAAAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGTCTG 60
Db 58 CAGGTACTCTGAAAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGTCTG 117
QY 61 ACTTGTTCTTCTCTGGTTTTCACGTAGCAGCACTCTGGTATGGGTGTGAGCTGGATTGCA 120

Db 118 ACTGTTCTTTCTCTGGTTTTCACGTGACACCTTCTGGTATGACCGTAGGTGGATTCGT 177
Qy 121 CAGCCTTCAGGAAGGGTCTGGAGTGGCTGGGCACACATTTACTTGGATGATGACAAAGCGC 180
Db 178 CAGCCTTCAGGAAGGGTCTGGAGTGGCTGGGCACACATTTGGTGAATGATGATAAGTAC 237
Qy 181 TATACCCATCCTGAAAGCGGCTTACATCTCCRAGGATACCTCCAGCAACAGGTA 240
Db 238 TATAACCCAGCCCTGAAAGCGGCTCAATCTCCAGGATACCTCCAAACACAGGTA 297
Qy 241 TTCTCTCAAGATCACCAGTGTGGACACTCGAGATAGTCCACATACTACTGTGCTCGAAGG 300
Db 298 TTCTCTCAAGATCACCAGTGTGGTCACTGAGATAGTCCACATACTACTGTGCTCGAAGG 357
Qy 301 GTCCTCTCAAGTGTGCTATGATGACTACTGGGTCAAGNACCTCACTACCGTCTCC 360
Db 358 GAGGAT---TACGACGAAGCTATGACTACTGGGTCAAGNACCTCACTACCGTCTCC 414
Qy 361 TCA 363
Db 415 TCA 417

RESULT 15
ID ABN84609
XX ABN84609 standard; cDNA; 465 BP.
XX AC ABN84609;
XX DT 29-OCT-2002 (first entry)
XX DE Anti-Streptococcus mutans surface antigen MAb SWLA2 VH coding region.
XX KW Streptococcus mutans; monoclonal antibody; MAb; mouse;
XX KW Chimeric antibody; antibody; anticaries; transgenic plant;
XX KW Transgenic animal; caries; immunotherapy; therapy; Gene; ss.
XX OS Mus musculus.
XX FH Key Location/Qualifiers
XX CDS 13..441
FT /*tag= a
FT /partial
FT /product= "SWLA2 heavy chain variable region"
FT /note= "the CDS does not include a stop codon"
XX PN
XX PN US2002068066-A1.
XX PD 06-JUN-2002.
XX PF 15-JUN-2001; 2001US-0881823.
XX PR 20-AUG-1999; 99US-0378577.
XX PA (SHIW/) SHI W.
XX PA (MORR/) MORRISON S L.
XX PA (TRIN/) TRINH K.
XX PA (WIMS/) WIMS L.
XX PA (CHEN/) CHEN L.
XX PA (ANDE/) ANDERSON M H.
XX PI Shi W, Morrison SL, Trinh K, Wims L, Chen L, Anderson MH;
XX DR WPI; 2002-565838/60.
XX DR P-PSDB; ABB79728.
XX PT Treatment and prevention of dental caries in mammals, in particular
XX PT humans by orally administering genetically engineered or purified
XX PT antibodies that bind to surface antigens of cariogenic organisms -
XX PS Claim 6; Fig 2B; 30pp; English.
XX XX

CC The present sequence is the coding sequence of the heavy chain
CC variable region (VH) of the murine monoclonal antibody SWLA2 (IgG),
CC which binds specifically to the surface antigens of cariogenic type
CC c Streptococcus mutans (ATCC 25175). The coding sequence was
CC obtained from SWLA2 (ATCC HB 12560) hybridoma cells by PCR
CC amplification (see also ABN84625 and ABN84622). The SWLA2 VH and
CC VL (see ABN84608) coding sequences were used in the preparation of
CC chimeric monoclonal antibody TEFE comprising SWLA2 variable regions
CC and human antibody constant regions. Such chimeric monoclonal
CC antibodies can be used to prevent or treat dental caries in humans.
CC The antibodies engage the effector apparatus of the human immune
CC system when they bind cariogenic organisms, resulting in their
CC destruction. The antibodies may be produced in edible plants,
CC in transgenic animals, or in chicken eggs for oral ingestion.
XX
SQ Sequence 465 BP; 108 A; 124 C; 113 G; 120 T; 0 other;

Query Match 78.3%; Score 284.4; DB 24; Length 465;
Best Local Similarity 88.0%; Pred. No. 1.4e-77;
Matches 322; Conservative 0; Mismatches 41; Indels 3; Gaps 1;

Qy 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGTCTG 60
Db 70 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGTCTG 129
Qy 61 ACTTGTCTTTCTCTCGGTTTTCACGTAGCACCTTCTGGTATGGGTGTGAGTGGATTGCA 120
Db 130 ACTTGTCTTTCTCTCGGTTTTCACGTAGAACCTTATGGTATAGGAGTAGGCTGGATTCT 189
Qy 121 CAGCCTTCAGGAAGGGTCTGGAGTGGCTGGGCACACATTTACTGGGATGATGACAAAGCGC 180
Db 190 CAGCCTTCAGGAAGGGTCTGGAGTGGCTGGGCACACATTTGGTGAATGATATAGTAC 249
Qy 181 TATAACCCATCCTCGAAGAGCCGGCTTACAATCTCCAAGGATACCTCCAGCAACCAAGGTA 240
Db 250 TATAACACAGTCTCTGAAGAGCCGGCTCACAACTCTCCAAGGATACCTCCAAACCAAGGTA 309
Qy 241 TTCTCTCAAGATCACCAGTGTGGACACTCGAGATAGTCCACATACTACTGTGCTCGAAGG 300
Db 310 TTCTCTCAAGATCACCAGTGTGGACACTCGAGATAGTCCACATACTACTGTGCTCGAAGG 369
Qy 301 GTCTCTCTAACTGCCT---ATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCAACCGTC 357
Db 370 GAGGGGGGCTCGGGCTACGATGTTATGGACTACTGGGGTCAAGGAATCTCAGTCAACCGTC 429
Qy 358 TCCTCA 363
Db 430 TCCTCA 435

Search completed: January 14, 2004, 16:03:11
Job time : 189.476 secs

High quality sequence stop: 451

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POLYA=No. Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
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/db_xref="niaEST:K0748C01-5N"
/db_xref="taxon:10090"
/clone="NIA:K0748C01 IMAGE:30078168"
/tissue_type="Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-)"
/dev stage="Age approx.10 weeks old"
/lab_host="DH10B"
/clone_lib="NIA Mouse Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-) cDNA Library (Long)"
/note="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were obtained from Drs. Dennis Taub, Dan Longo (National Cancer Institute on Aging, USA), Jonathan Keller (National Cancer Institute, USA). Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 5'-pGACTAGTTCGAGCGCGCCCTTTT-3'] from 0.9 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker LI-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and NotI enzymes. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.1 kb. The library was constructed by Yulan Piao (NIA)."
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BASE COUNT 99 a 129 c 104 g 119 t

ORIGIN

Query Match 88.9%; Score 322.8; DB 14; Length 451;
 Best Local Similarity 94.5%; Pred. No. 6e-84;
 Matches 346; Conservative 0; Mismatches 17; Indels 3; Gaps 1;

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Qy 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTCAGAGCCCTCCAGACCCCTCAGTCTG 60
Db 38 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTCAGGTCCTCCAGACCCCTCAGTCTG 97
Qy 61 ACTTGTTCTTCTCTGGTTTCTACTGAGCACTCTCGTATGGGTGAGCTGAGCTGATCGA 120
Db 98 ACTTGTTCTTCTCTGGTTTCTACTGAGCACTCTCGTATGGGTGAGCTGAGCTGATCGT 157
Qy 121 CAGCCTTCAGGAAGGCTCTGAGTGGCTGGCAGACATTTACTGGGATGATGACAGCGC 180
Db 158 CAGCCTTCAGGAAGGCTCTGAGTGGCTGGCAGACATTTACTGGGATGATGACAGCGC 217
Qy 181 TATAACCATCTCCGAGAGCGGCTTACATCTCCAGGATACCTCCAGCAACCGGTA 240
Db 218 TATAACCATCTCCGAGAGCGGCTTACATCTCCAGGATACCTCCAGCAACCGGTA 277
Qy 241 TTCCTCAAGTACACAGTGGGACCTCGAGATCTGCCACATCTACTGTGTC---GA 297
Db 278 TTCCTCAAGTACACAGTGGGACCTCGAGATCTGCCACATCTACTGTGTCGAGAG 337
Qy 298 AGGCTCTCTTAACCTGCTATGCTATGCTATGCTGCGGTCAAGGAACCTCAGTCACCGTC 357
Db 338 AGTGAATACCTCCATATGCTATGCTATGCTATGCTGCGGTCAAGGAACCTCAGTCACCGTC 397
358 TCCTCA 363
|||||

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Db 398 TCCTCA 403

RESULT 2

CA578844

LOCUS

DEFINITION

K0729C06-5N NIA Mouse Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-) cDNA Library (Long) Mus musculus cDNA clone NIA:K0729C06 IMAGE:30076349 5', mRNA sequence.

CA578844

ACCESSION

CA578844

VERSION

CA578844.1

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

1 (bases 1 to 485)

AUTHORS

Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Carter, M.G., Alba, K., Taub, D., Longo, D.L., Keller, J. and Ko, M.S.H.

TITLE

Systematic Analyses of NIA Mouse Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-) cDNA Library (Long)

JOURNAL

Unpublished

COMMENT

Other ESTs: K0729C06-3

Contact: Dawood B. Dudekula

Laboratory of Genetics

National Institute on Aging/National Institutes of Health

333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA

Email: cdna@lgsun.grc.nia.nih.gov

Plate: K0729 row: C column: 06

Seq primer: M13 Reverse

High quality sequence stop: 485

POLYA=No.

Location/Qualifiers

1. .485

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6Ncr"

/db_xref="niaEST:K0729C06-5N"

/db_xref="taxon:10090"

/clone="NIA:K0729C06 IMAGE:30076349"

/tissue_type="Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-)"

/dev stage="Age approx.10 weeks old"

/lab_host="DH10B"

/clone_lib="NIA Mouse Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-) cDNA Library (Long)"

/note="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were obtained from Drs. Dennis Taub, Dan Longo (National Cancer Institute on Aging, USA), Jonathan Keller (National Cancer Institute, USA). Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 5'-pGACTAGTTCGAGCGCGCCCTTTT-3'] from 0.9 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker LI-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and NotI enzymes. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.1 kb. The library was constructed by Yulan Piao (NIA)."

BASE COUNT 105 a 138 c 114 g 128 t

ORIGIN

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Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"

BASE COUNT      171 a      260 c      222 g      211 t
ORIGIN
Query Match      83.4%; Score 302.6; DB 10; Length 864;
Best Local Similarity 92.2%; Pred. No. 6.6e-78;
Matches 344; Conservative 0; Mismatches 19; Indels 10; Gaps 2;

QY 1 CAGGTTACTCTGAAGAAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCCCTCAGTCTG 60
Db 38 CAGGTTACTCTGAAGAAGTCTGGCCCTGGGATATTCAGTCCCTCCAGACCCCTCAGTCTG 97
QY 61 ACTTGTTCTTCTCTGGTCTTCACTGAGCAGCTTCTGGTATGCTGGTGTGAGCTGGATTGGA 120
Db 98 ACTTGTTCTTCTCTGGTCTTCACTGAGCAGCTTCTGGTATGCTGGTGTGAGCTGGATTGCT 157
QY 121 CAGCCTTCAGAAAGGCTCTGAGTGGCTGGCCACACATTTACTGGGATGATGACAAGCGC 180
Db 158 CAGCCTTCAGAAAGGCTCTGAGTGGCTGGCCACACATTTACTGGGATGATGACAAGCGC 217
QY 181 TATAACCCATCCCTGAGAGCGGCTTACATCTCCAGGATACCTCCAGACACAGGTA 240
Db 218 TATAACCCATCCCTGAGAGCGGCTTACATCTCCAGGATACCTCCAGAAACCAAGGTA 277
QY 241 TTCTCTAAGATCACCACTGTGGACACTCGAGATCTGCCACATCTACTGTGCTC---GA 297
Db 278 TTCTCTAAGATCACCACTGTGGACACTCGAGATCTGCCACATCTACTGTGCTCGAGA 337
QY 298 AGGCTCTCTACTGCTGCTATGCTATGAGTACTGGGGTCAAGAACCTCAGTCACCGTC 357
Db 338 AGTGAATACCCCTCATACTATGCTATGAGTACTGGGGTCAAGAACCTCAGTCACCGTC 397
QY 358 TCCTCA 363
Db 398 TCCTCA 403

RESULT 3
BE309336      864 bp      mRNA      linear      EST 26-OCT-2000
LOCUS      601093720P1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3488309 5',
DEFINITION      mRNA sequence.
ACCESSION      BE309336
VERSION      BE309336.1 GI:9167366
KEYWORDS      EST.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished
COMMENT      Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM8527 row: h column: 06
High quality sequence stop: 645.
Location/Qualifiers
1..864
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/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:3488309"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP Mam5"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site:1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.

Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"

BASE COUNT      171 a      260 c      222 g      211 t
ORIGIN
Query Match      83.4%; Score 302.6; DB 10; Length 864;
Best Local Similarity 92.2%; Pred. No. 6.6e-78;
Matches 344; Conservative 0; Mismatches 19; Indels 10; Gaps 2;

QY 1 CAGGTTACTCTGAAGAAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCCCTCAGTCTG 60
Db 43 CAGGTTACTCTGAAGAAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCCCTCAGTCTG 102
QY 61 ACTTGTTCTTCTCTGGTCTTCACTGAGCAGCTTCTGGTATGCTGGTGTGAGCTGGATTGCG 119
Db 103 ACTTGTTCTTCTCTGGTCTTCACTGAGCAGCTTCTCATATTTACTGGTGTGAGCTGGATTGCG 162
QY 120 ACAGCCTTCAGAAAGGCTCTGGAGTGGCTGGCCACACATTTACTGGGATGATGACAAGCG 179
Db 163 TCAGCCTTCAGAAAGGCTCTGGAGTGGCTGGCCACACATTTACTGGGATGATGACAAGCG 222
QY 180 CTATAACCCATCCCTGAGAGCGGCTTACATCTCCAGGATACCTCCAGCAACCAAGGT 239
Db 223 CTATAACCCATCCCTGAGAGCGGCTTACATCTCCAGGATACCTCCAGCAACCAAGGT 282
QY 240 ATTCTCTAAGATCACCACTGTGGACACTCGAGATCTGCCACATCTACTGTGCTCGAAG 299
Db 283 ATTCTCTAAGATCACCACTGTGGACACTCGAGATCTGCCACATCTACTGTGCTCGAAT 342
QY 300 GGTCTCTCTAACTG-----CCTATGCTATGAGTACTGGGGTCAAGAACCTCAGT 350
Db 343 TTATTACCACCGTGTGATGCTTACTATGCTATGAGTACTGGGGTCAAGAACCTCAGT 402
QY 351 CACCGCTCTCTCA 363
Db 403 CACCGCTCTCTCA 415

RESULT 4
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LOCUS      602098016P1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4218099 5',
DEFINITION      mRNA sequence.
ACCESSION      BE309336
VERSION      BE309336.1 GI:11656827
KEYWORDS      EST.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished
COMMENT      Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM9797 row: p column: 04
High quality sequence stop: 656.
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4218099"

FEATURES
source
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/lab_host="PH108 (T1 phage-resistant)"

/clone_lib="NCI_CGAP_Co24"

/note="Organ: colon; Vector: pCMV-SPORT6; Site: 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 183 a 261 c 250 g 219 t

ORIGIN

Query Match 82.8%; Score 300.6; DB 10; Length 913;
Best Local Similarity 90.5%; Pred. No. 2.6e-77;
Matches 334; Conservative 0; Mismatches 29; Indels 6; Gaps 1;
QY 1 CAGGTTACTCTGAAGAGCTGSCCTGGGATATTGACGCTCCAGACCCCTCAGTCTG 60
DB 60 CAGGTTACTCTGAAGAGCTGSCCTGGGATATTGACGCTCCAGACCCCTCAGTCTG 119
QY 61 ACTTGTCTTTCTCTGGTTTCACTGACACCTTCTGGTATGGGTGAGTGGATTGGA 120
DB 120 ACTTGTCTTTCTCTGGTTTCACTGACACCTTCTGGTATGGGTGAGTGGATTGGA 179
QY 121 CAGCCTTCAGGAAGGCTCTGGAGTGGCTGGCACACATTTACTGGGATGACAAAGCC 180
DB 180 CAGCCTTCAGGAAGGCTCTGGAGTGGCTGGCACACATTTACTGGGATGACAAAGCC 239
QY 181 TATAACCCATCCCTGAAGAGCGGCTTACAATCTCCAGGATACCTCCAGCAACAGGTA 240
DB 240 TATAACCCATCCCTGAAGAGCGGCTTACAATCTCCAGGATACCTCCAGCAACAGGTA 299
QY 241 TTCTCAAGATCACCAGTGGGACCTGAGATGCTGACATCTGACATCTGCTGCTCG --- 296
DB 300 TTCTCAAGATCACCAGTGGGACCTGAGATGCTGACATCTGACATCTGCTGCTCG 359
QY 297 --AAGGCTCTCTAACTGCTATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 354
DB 360 TATGATGTTACCATATTACTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 419
QY 355 GTCTCTCTCA 363
DB 420 GTCTCTCTCA 428

RESULT 5
BG963642 602828443F1 NCI_CGAP_Co24 Mus musculus cdna clone IMAGE:4983155 5',
LOCUS BG963642 mRNA sequence.
DEFINITION BG963642.1 GI:14351279
ACCESSION BG963642
VERSION BG963642.1
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 666)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapsb-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM10987 row: e column: 12
High quality sequence stop: 658.
Location/Qualifiers
1. 666
/organism="Mus musculus"
/mol_type="mRNA"

FEATURES
source

/strain="FVB/N"

/db_xref="taxon:10090"

/clone_lib="NCI_CGAP_Co24"

/lab_host="PH108 (T1 phage-resistant)"

/note="Organ: colon; Vector: pCMV-SPORT6; Site: 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 157 a 186 c 159 g 164 t

Query Match 82.3%; Score 298.6; DB 12; Length 666;
Best Local Similarity 91.5%; Pred. No. 9e-77;
Matches 343; Conservative 0; Mismatches 19; Indels 13; Gaps 2;
QY 1 CAGGTTACTCTGAAGAGCTGSCCTGGGATATTGACGCTCCAGACCCCTCAGTCTG 60
DB 59 CAGGTTACTCTGAAGAGCTGSCCTGGGATATTGACGCTCCAGACCCCTCAGTCTG 117
QY 61 ACTTGTCTTTCTCTGGTTTCACTGACACCTTCTGGTATGGGTGAGTGGATTGGA 120
DB 118 ACTTGTCTTTCTCTGGTTTCACTGACACCTTCTGGTATGGGTGAGTGGATTGGA 177
QY 121 CAGCCTTCAGGAAGGCTCTGGAGTGGCTGGCACACATTTACTGGGATGACAAAGCC 180
DB 178 CAGCCTTCAGGAAGGCTCTGGAGTGGCTGGCACACATTTACTGGGATGACAAAGCC 237
QY 181 TATAACCCATCCCTGAAGAGCGGCTTACAATCTCCAGGATACCTCCAGCAACAGGTA 240
DB 238 TATAACCCATCCCTGAAGAGCGGCTTACAATCTCCAGGATACCTCCAGCAACAGGTA 297
QY 241 TTCTCAAGATCACCAGTGGGACCTGAGATGCTGACATCTGACATCTGCTGCTCG --- 296
DB 298 TTCTCAAGATCACCAGTGGGACCTGAGATGCTGACATCTGACATCTGCTGCTCG 357
QY 297 -----AAGGCTCTCTAACTGCTATGCTATGCTATGCTATGCTATGCTATGCTAT 348
DB 358 TATAGTTACTATAGTTAGGAATATTACTATGCTATGCTATGCTATGCTATGCTATG 417
QY 349 GTCAACGCTCTCTCA 363
DB 418 GTCAACGCTCTCTCA 432

RESULT 6
BF178694 601806679F1 NCI_CGAP_Mam5 Mus musculus cdna clone IMAGE:4037587 5',
LOCUS BF178694 mRNA sequence.
DEFINITION BF178694.1 GI:11056836
ACCESSION BF178694
VERSION BF178694.1
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 940)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapsb-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM9314 row: n column: 20
High quality sequence stop: 631.
Location/Qualifiers

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LAM10985 row: 1 column: 06
High quality sequence stop: 648.
Location/Qualifiers
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/db_xref="taxon:10090"
/clone="IMAGE:4982549"
/lab_host="DH10B (Tl phage-resistant)"
/clone_lib="NCI_CGAP_Co24"
/note="Organ: colon; Vector: pCMV-Sport6; Site: 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 Kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 141 a 184 c 163 g 164 t
ORIGIN
Query Match 77.5%; Score 281.4; DB 12; Length 652;
Best Local Similarity 86.0%; Pred. No. 1e-71;
Matches 312; Conservative 0; Mismatches 51; Indels 0; Gaps 0;
QY 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCTCAGTCTG 60
Db CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCTCAGTCTG 112
QY 61 ACTTGTCTTTCTCTGGTTTTCACAGACCTCTGGTATGGTGTGAGCTGGATTGGA 120
Db ACTTGTCTTTCTCTGGTTTTCACAGACCTCTGGTATGGTGTGAGCTGGATTGGA 172
QY 121 CAGCCTTCAGGAAGGCTCTGGATGGCTGGACACATTTACTGGATGATGCAAGCGC 180
Db CAGCCTTCAGGAAGGCTCTGGATGGCTGGACACATTTACTGGATGATGCAAGCGC 232
QY 173 CAGCCTTCAGGAAGGCTCTGGATGGCTGGACACATTTACTGGATGATGCAAGCGC 240
Db CAGCCTTCAGGAAGGCTCTGGATGGCTGGACACATTTACTGGATGATGCAAGCGC 292
QY 181 TATAATCCATCCCTGAAGACCCGGCTTACAATCTCAAGGATACCTCCAGCAACAGGTA 300
Db TATAATCCATCCCTGAAGACCCGGCTTACAATCTCAAGGATACCTCCAGCAACAGGTA 352
QY 241 TTCTCAAGATCACAGTGTGGACACTCGAGATCTGCCACATCTACTGTGCTGAGG 360
Db TTCTCAAGATCACAGTGTGGACACTCGAGATCTGCCACATCTACTGTGCTGAGG 412
QY 301 GTCTCTTAATCTGCTATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCCCGTCC 360
Db GTCTCTTAATCTGCTATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCCCGTCC 412
QY 361 TCA 363
Db 413 TCA 415
RESULT 9
AW989547 391 bp mRNA linear EST 02-JUN-2000
LOCUS ug14h06.y1 Soares_mammary_gland_NMLMG_Mus_musculus_cDNA_clone
DEFINITION IMAGE:1531643 5' similar to SW:EV2H HUMAN P04438 IG HEAVY CHAIN
V-II REGION SESS PRECURSOR. [1] ;, mRNA sequence.
ACCESSION AW989547
VERSION AW989547.1 GI:8184975
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 391)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cyabps-remail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:947743
Trace considered overall poor quality
Seq primer: -40RP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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/sex="female (lactating)"
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BASE COUNT 88 a 107 c 90 g 106 t
ORIGIN
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Best Local Similarity 95.0%; Pred. No. 8.2e-71;
Matches 287; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
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Db CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTCAGCTCTCCAGACCTCAGTCTG 115
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QY 121 CAGCCTTCAGGAAGGCTCTGGATGGCTGGACACATTTACTGGATGATGCAAGCGC 180
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Db TAGCCTTCACGAAGGCTCTGGATGGCTGGACACATTTACTGGATGATGCAAGCTT 295
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Db TATAACCCATCCCTGAAGAGCCGGCTTACAATCTCAAGGATACCTCCAGCAACAGGTA 355
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QY 301 GT 302
Db 356 GT 357
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LOCUS K0731E07-SN NIA Mouse Hematopoietic Stem Cell (Lin-/c-kit-/Sca-1-)
DEFINITION CDNA Library (Long) Mus musculus cDNA clone NIA:K0731E07
IMAGE:30076566 5' ;, mRNA sequence.
ACCESSION CA579006
VERSION CA579006.1 GI:25127397
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 485)
 Piaoy.Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Carter, M.G.,
 Aliba, K., Taub, D., Longo, D.L., Keller, J. and Ko, M.S.H.
 Systematic Analyses of NIA Mouse Hematopoietic Stem Cell
 (Lin-/c-Kit-/Sca-1-) cDNA Library (Long)
 Unpublished
 Other ESTs: K0731E07-3
 Contact: Dawood B. Dudekula
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
 Email: cdna@lgsun.grc.nia.nih.gov
 Plate: K0731 row: E column: 07
 Seq primer: M13 Reverse
 High quality sequence stop: 485
 POLYA=No.

FEATURES

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 /notes="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2:
 NotI; Mouse cDNA project by the Laboratory of Genetics,
 National Institute on Aging (NIA), Intramural Research
 Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is
 a long-transcript enriched cDNA library (Ref. Genome Res.
 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were
 obtained from Drs. Dennis Taub, Dan Longo (National
 Institute on Aging, USA), Jonathan Keller (National Cancer
 Institute, USA). Double-stranded cDNAs were synthesized
 with an oligo(dT) primer [Invitrogen]:
 5'-pGATCTACTGATCGAGCGCGCCCTCTTTT-3' from
 0.9 ug of total RNA, treated with T4 DNA polymerase, and
 purified by ethanol-precipitation. The cDNAs were ligated
 to Lona-linker IL-Sal4, purified by phenol/chloroform, and
 separated from free linkers by Centricon 100. Then, the
 cDNAs were amplified by long-range high fidelity PCR using
 Ex Taq polymerase (Takara) with a primer Sal4-S. The
 products were purified by phenol/chloroform and Centricon
 100. The cDNAs were digested with SalI and NotI enzymes
 and cloned into SalI/NotI site of pSPORT1 plasmid vector.
 The DH10B E. coli host was transformed with the ligation
 mixture by the standard chemical method. The average
 insert size is about 2.1 kb. The library was constructed
 by Yulan Piao (NIA)."
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BASE COUNT

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 Matches 316; Conservative 0; Mismatches 47; Indels 6; Gaps 1;

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Db

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QY

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Db

95 ACTTGTCTTCTCTGGTCTTTCACCTGAGCACTCTGGTATGGTGTGAGCTGGATTCA 154

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121 CAGCCTTCAGGAAGGCTCTGGAGTGGCTGGCCACACATTACTGGGATGATCACAAGCCG 180

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 cDNA Library (Long) Mus musculus cDNA clone NIA:K0733C10
 IMAGE:30076737 5', mRNA sequence.

ACCESSION

CA579140

VERSION

CA579140.1 GI:25127531

KEYWORDS

EST.

ORGANISM

Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 485)

AUTHORS

Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Carter, M.G.,
 Aliba, K., Taub, D., Longo, D.L., Keller, J. and Ko, M.S.H.

TITLE

Systematic Analyses of NIA Mouse Hematopoietic Stem Cell
 (Lin-/c-Kit-/Sca-1-) cDNA Library (Long)

JOURNAL

Unpublished

COMMENT

Other ESTs: K0733C10-3
 Contact: Dawood B. Dudekula
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
 Email: cdna@lgsun.grc.nia.nih.gov
 Plate: K0733 row: C column: 10
 Seq primer: M13 Reverse
 High quality sequence stop: 485
 POLYA=No.

FEATURES

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 /organism="Mus musculus"
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 (Lin-/c-Kit-/Sca-1-) cDNA Library (Long)"
 /note="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2:
 NotI; Mouse cDNA project by the Laboratory of Genetics,
 National Institute on Aging (NIA), Intramural Research
 Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is
 a long-transcript enriched cDNA library (Ref. Genome Res.
 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were
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 cDNAs were amplified by long-range high fidelity PCR using
 Ex Taq polymerase (Takara) with a primer Sal4-S. The
 products were purified by phenol/chloroform and Centricon
 100. The cDNAs were digested with SalI and NotI enzymes
 and cloned into SalI/NotI site of pSPORT1 plasmid vector.
 The DH10B E. coli host was transformed with the ligation
 mixture by the standard chemical method. The average
 insert size is about 2.1 kb. The library was constructed
 by Yulan Piao (NIA)."

COMMENT

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh
M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunura
S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
e mouse tissues.

FEATURES

source

Location/Qualifiers

1..379
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/mol_type="mRNA"
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Query Match 73.7%; Score 267.6; DB 10; Length 379;
Best Local Similarity 93.6%; Pred. No. 9.1e-68;
Matches 279; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
Qy 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCAGTCTG 60
Db 79 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCAGTCTG 138
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Qy 241 TTCTTCAAGATCACCGATGGGACACTCGAGACTGCGCATACTACTGTGCTGAA 298
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RESULT 14

CAS78658

LOCUS

DEFINITION

K0726H06-5N NIA Mouse Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-)
428 bp mRNA linear EST 19-NOV-2002

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES

source

Location/Qualifiers

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(Lin-/c-Kit-/Sca-1-) cDNA Library (Long)"
/note="vector: pSPORT1 (Invitrogen); Site1: SalI; Site2:
NotI; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is
a long-transcript enriched cDNA library (Ref. Genome Res.
11: 1553-1558 (2001)). [PMID: 11544199]. Total RNAs were
obtained from Drs. Dennis Taub, Dan Longo (National Cancer
Institute, USA), Jonathan Keller (National Cancer
Institute, USA). Double-stranded cDNAs were synthesized
with an Oligo(dT) primer (Invitrogen):
5'-PGACTAGTCTAGATCGAGCGCCGCTTTT-3' from
0.9 ug of total RNA, treated with T4 DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to lone-linker L1-SalI, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer SalI-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of pSPORT1 plasmid vector.
The DH10B E. coli host was transformed with the ligation
mixture by the standard chemical method. The average
insert size is about 2.1 kb. The library was constructed
by Yulan Piao (NIA)."

BASE COUNT

ORIGIN

Query Match 73.2%; Score 265.8; DB 14; Length 428;
Best Local Similarity 87.1%; Pred. No. 3.2e-67;
Matches 304; Conservative 0; Mismatches 42; Indels 3; Gaps 1;
Qy 15 AGAGTCTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCAGTCTGACTGTTCTTC 74
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cDNA library (Long) Mus musculus cDNA clone NIA:K0726H06
IMAGE:30076121 5', mRNA sequence.

CAS78658
CA578658.1 GI:25127049
EST.

Mus musculus (house mouse)

Mus musculus

1 (bases 1 to 428)
Fiao, Y., Kargul, G. J., Dudekula, D. B., Qian, Y., Luo, A., Carter, M. G.,
Alba, K., Taub, D., Longo, D. L., Keller, J. and Ko, M. S. H.
Systematic Analyses of NIA Mouse Hematopoietic Stem Cell
(Lin-/c-Kit-/Sca-1-) cDNA Library (Long)
Unpublished
Other ESTs: K0726H06-3

Contact: Dawood B. Dudekula

Laboratory of Genetics

National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6920, USA
Email: cdna@lgsun.grc.nia.nih.gov

Plate: K0726 row: H column: 06

Seq primer: M13 Reverse

High quality sequence stop: 428

POLYA-No.

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 BB870162.1 GI:17116372
 Mus musculus (house mouse)
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 1 (bases 1 to 363)
 Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T.,
 Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii
 Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T.,
 Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T.,
 Saigo, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,
 Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa
 A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T.,
 Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
 RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
 2001)

Unpublished
 Contact: Yoshinhide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gs.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh
 M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
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 wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
 Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura
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 RIKEN integrated sequence analysis (RISA) system--384-format
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 10 (11), 1757-1771 (2000)
 Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
 Y. and Hayashizaki, Y.
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for

further details.

e mouse tissues.
 Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="mRNA"
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 Best Local Similarity 93.5%; Pred. No. 2.6e-66;
 Matches 274; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
 QY 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGTCTG 60
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Job time : 1468.4 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)
3641.411 Million cell updates/sec

Title: US-09-759-112A-5

Perfect score: 363

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	299.2	82.4	738	1	US-08-197-834-6
6	296.4	81.7	417	5	PCT-US95-07372-9
7	291	80.2	418	2	US-08-553-501A-28
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9	261.8	72.1	462	1	US-08-436-463-1
10	250.8	69.1	812	1	US-08-408-133-1
11	250.8	69.1	812	1	US-08-454-683-1
12	250.8	69.1	812	2	US-08-116-7783-16
13	250.8	69.1	812	2	US-08-454-680-1
14	250.8	69.1	812	2	US-08-438-562-16
15	250.8	69.1	812	2	US-08-483-528B-16
16	250.8	69.1	812	3	US-08-673-799C-16
17	250.8	69.1	812	4	US-09-393-385B-16
18	250.8	69.1	812	4	US-09-225-322B-1
19	250.8	69.1	812	4	US-09-764-304-1
20	191.4	52.7	423	4	US-08-561-309-50
21	190.6	52.5	423	2	US-08-345-321-9
22	190.2	52.4	613	3	US-08-545-809A-5
23	185.4	51.1	418	3	US-08-553-501A-58
24	185.4	51.1	418	3	US-09-205-231-58
25	185.4	51.1	1607	3	US-09-049-672A-14
26	183.8	50.6	418	2	US-08-553-501A-60
27	183.8	50.6	418	3	US-09-205-231-60

28	181.2	49.9	546	3	US-08-545-809A-26	Sequence 26, Appl
29	172.6	47.5	630	3	US-08-545-809A-10	Sequence 10, Appl
30	171	47.1	423	2	US-08-483-636-11	Sequence 11, Appl
31	171	47.1	423	2	US-08-483-632-11	Sequence 11, Appl
32	168.4	46.4	646	4	US-09-702-705-1113	Sequence 1113, Ap
33	168.4	46.4	646	4	US-09-736-457-1113	Sequence 1113, Ap
34	165	45.5	714	4	US-09-142-974B-2	Sequence 2, Appl
35	165	45.5	1173	4	US-09-142-974B-4	Sequence 4, Appl
36	163.2	45.0	378	1	US-08-488-376-15	Sequence 15, Appl
37	163.2	45.0	378	2	US-08-634-223-15	Sequence 15, Appl
38	163.2	45.0	378	2	US-08-634-224-15	Sequence 15, Appl
39	163.2	45.0	378	2	US-08-634-400-15	Sequence 15, Appl
40	163.2	45.0	378	2	US-08-635-878-15	Sequence 15, Appl
41	163.2	45.0	378	2	US-08-770-057-15	Sequence 15, Appl
42	163.2	45.0	378	3	US-09-335-697B-15	Sequence 15, Appl
43	163.2	45.0	378	4	US-09-335-697B-15	Sequence 15, Appl
44	163.2	45.0	378	4	US-09-740-002-15	Sequence 15, Appl
45	163.2	45.0	1428	1	US-08-488-376-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-08-483-636-3
; Sequence 3, Application US/08483636
; Patent No. 5914110
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/483,636
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 483 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown

MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 64..483
US-08-483-632-3

Query Match 86.3%; Score 313.4; DB 2; Length 483;
Best Local Similarity 91.5%; Pred. No. 7.1e-99;
Matches 332; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY	1	CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGCGACCTCCAGACCCCTCAGTCTG	60
DB	121	CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGCGACCTCCAGACCCCTCAGTCTG	180
QY	61	ACTGTGTTCTTCTCTGGGTTTTCACGTGACACTTCTGGTATGGGTGTGAGTGGATTGGA	120
DB	181	ACTGTGTTCTTCTCTGGGTTTTCACGTGACACTTCTGGTATGGGTGTGAGTGGATTGGA	240
QY	121	CAGCCTTCAGGAAAGGTTCTGGAGTGGCTGGGCACACATTTACTGGGATGATGACAAGGC	180
DB	241	CAGCCTTCAGGAAAGGTTCTGGAGTGGCTGGGCACACATTTACTGGGATGATGACAAGGC	300
QY	181	TATAACCCATCCCTGAAGAGCGGCTTACAATCTCAAGGATACCTCCAGCAACAGGTA	240
DB	301	TATAACCCATCCCTGAAGAGCGGCTTACAATCTCAAGGATACCTCCAGCAACAGGTA	360
QY	241	TTCTCAAGATCACCAGTGTGACACTCGAGATCTGCCACATCTACTGTCTCGAAGG	300
DB	361	TTCTCAAGATCACCAGTGTGACACTCGAGATCTGCCACATCTACTGTCTCGAAGG	420
QY	301	GTCTCTTAACCTGCTATGCTATGAGTACTGGGTCAAGAACTCAGTCAAGTCTCC	360
DB	421	GAGACTGTGTTCTTCTGTTCTGATGTTCTGGGCGGAGGACCAAGTCAAGTCTCC	480
QY	361	TCA 363	
DB	481	TCA 483	

RESULT 2

US-08-483-632-3
Sequence 3, Application US/08483632
Patent No. 5928904
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
TREATMENT OF IL4 Mediated Disorders
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESS: Intellectual Property
STREET: P.O. Box 1539 / UW2220
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,632
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 483 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 64..483
US-08-483-632-3

Query Match 86.3%; Score 313.4; DB 2; Length 483;
Best Local Similarity 91.5%; Pred. No. 7.1e-99;
Matches 332; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY	1	CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGCGACCTCCAGACCCCTCAGTCTG	60
DB	121	CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGCGACCTCCAGACCCCTCAGTCTG	180
QY	61	ACTGTGTTCTTCTCTGGGTTTTCACGTGACACTTCTGGTATGGGTGTGAGTGGATTGGA	120
DB	181	ACTGTGTTCTTCTCTGGGTTTTCACGTGACACTTCTGGTATGGGTGTGAGTGGATTGGA	240
QY	121	CAGCCTTCAGGAAAGGTTCTGGAGTGGCTGGGCACACATTTACTGGGATGATGACAAGGC	180
DB	241	CAGCCTTCAGGAAAGGTTCTGGAGTGGCTGGGCACACATTTACTGGGATGATGACAAGGC	300
QY	181	TATAACCCATCCCTGAAGAGCGGCTTACAATCTCAAGGATACCTCCAGCAACAGGTA	240
DB	301	TATAACCCATCCCTGAAGAGCGGCTTACAATCTCAAGGATACCTCCAGCAACAGGTA	360
QY	241	TTCTCAAGATCACCAGTGTGACACTCGAGATCTGCCACATCTACTGTCTCGAAGG	300
DB	361	TTCTCAAGATCACCAGTGTGACACTCGAGATCTGCCACATCTACTGTCTCGAAGG	420
QY	301	GTCTCTTAACCTGCTATGCTATGAGTACTGGGTCAAGAACTCAGTCAAGTCTCC	360
DB	421	GAGACTGTGTTCTTCTGTTCTGATGTTCTGGGCGGAGGACCAAGTCAAGTCTCC	480
QY	361	TCA 363	
DB	481	TCA 483	

RESULT 3

US-08-483-636-9
Sequence 9, Application US/08483636
Patent No. 5914110
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
TREATMENT OF IL4 Mediated Disorders
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESS: Intellectual Property
STREET: P.O. Box 1539 / UW2220
CITY: King of Prussia
STATE: PA
COUNTRY: USA

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; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483.636
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 423 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..423
; US-08-483-636-9

Query Match      85.9%; Score 311.8; DB 2; Length 423;
Best Local Similarity 91.2%; Pred. No. 2.4e-98;
Matches 331; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY      1  CAGGTTACTCTGAAGAGCTCTGGCCCTGGGATATTGCAGCCCTCCAGACCCCTCAGTCTG 60
DB      61  CAGGTTACCTTGAAGAGCTCTGGCCCTGGGATATTGCAGCCCTCCAGACCCCTCAGTCTG 120

QY      61  ACTTGTTCTTTCTCTGGGTTTCTACTGAGCACTTCTGTTGGTGTGAGCTGGATTCGA 120
DB      121  ACTTGTTCTTTCTCTGGGTTTCTACTGAGCACTTCTGTTGGTGTGAGCTGGATTCGT 180

QY      121  CAGCCTTCAGGAAGGGTCTGGAGTGGCTGGCACACATTTTACTGGGATGATGACAAGCGC 180
DB      181  CAGCCTTCAGGAAGGGTCTGGAGTGGCTGGCACACATTTTACTGGGATGATGACAAGCGC 240

QY      181  TATAACCATCCCTGAAGAGCGGCTTACATCTCCAGGATACCTCCAGCAACAGGTA 240
DB      241  TATAACCATCCCTGAAGAGCGGCTTACATCTCCAGGATACCTCCAGCAACAGGTA 300

RESULT 4
US-08-483-632-9

; Sequence 9, Application US/08483632
; Patent No. 5928904
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483.632
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 423 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..423
; US-08-483-632-9

Query Match      85.9%; Score 311.8; DB 2; Length 423;
Best Local Similarity 91.2%; Pred. No. 2.4e-98;
Matches 331; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY      1  CAGGTTACTCTGAAGAGCTCTGGCCCTGGGATATTGCAGCCCTCCAGACCCCTCAGTCTG 60
DB      61  CAGGTTACCTTGAAGAGCTCTGGCCCTGGGATATTGCAGCCCTCCAGACCCCTCAGTCTG 120

QY      61  ACTTGTTCTTTCTCTGGGTTTCTACTGAGCACTTCTGTTGGTGTGAGCTGGATTCGA 120
DB      121  ACTTGTTCTTTCTCTGGGTTTCTACTGAGCACTTCTGTTGGTGTGAGCTGGATTCGT 180

QY      121  CAGCCTTCAGGAAGGGTCTGGAGTGGCTGGCACACATTTTACTGGGATGATGACAAGCGC 180
DB      181  CAGCCTTCAGGAAGGGTCTGGAGTGGCTGGCACACATTTTACTGGGATGATGACAAGCGC 240

QY      181  TATAACCATCCCTGAAGAGCGGCTTACATCTCCAGGATACCTCCAGCAACAGGTA 240
DB      241  TATAACCATCCCTGAAGAGCGGCTTACATCTCCAGGATACCTCCAGCAACAGGTA 300
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QY 241 TTCTCAAGATCACCAGTGTGGACACTCGAGTACTGCGACATACATCTACTGTCTCGAGG 300
Db 301 TTCTCAAGATCACCAGTGTGGACACTCGAGTACTGCGACATACATCTACTGTCTCGAAGA 360
QY 301 GTCCTCTAACTGCCCTATCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCC 360
Db 361 GAGACTGTCTTCTACTGTGGTACTTGGATGTCTGGGGCGCAGGACACACGGTCAACGCTCTCC 420
QY 361 TCA 363
Db 421 TCA 423

RESULT 5

US-08-197-834-6
; Sequence 6, Application US/08197834
; Patent No. 5639455
; GENERAL INFORMATION:
; APPLICANT: SHIMAMURA, TOSHIRO
; APPLICANT: NAKAZAWA, HARUMI
; APPLICANT: HAMURO, JUNJI
; TITLE OF INVENTION: IMMUNOSUPPRESSANT
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,834
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER: JP 028173/1993
; FILING DATE: 17-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5639455man P.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-661-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 738 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid;
; DESCRIPTION: DNA (synthetic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..738
; US-08-197-834-6

Query Match 82.4%; Score 299.2; DB 1; Length 738;
Best Local Similarity 90.1%; Pred. No. 7.3e-94;
Matches 335; Conservative 0; Mismatches 28; Indels 9; Gaps 1;
QY 1 CAGGTACTCTGAAGAGTCTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCAGTCTG 60
Db 367 CAGGTCAACTCGAGGAGTCTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCAGTCTG 426

QY 61 ACTTGTTCTTCTCTCGGTTTTCACGTAGCAGCTTCTGGTATGGGTGTGAGCTGGATTCA 120
Db 427 ACTTGTTCTTCTCTCGGTTTTCACGTAGCAGCTTCTGGTATGGGTGTGAGCTGGATTCT 486
QY 121 CAGCCTTCAGGAAGGGTCTGGAGTGGCTGGGACACATTTACTGGGATGATGACAAAGCGC 180
Db 487 CAGCCTTCAGGAAGGGTCTGGAGTGGCTGGGACACATTTACTGGGATGATGACAAACAC 546
QY 181 TATAAACCATCCCTGAAGAGCGGCTTTACAATCTCCAAGGTACTCTCCAGCAACACAGGTA 240
Db 547 TATAAACCATCCCTGAAGAGCGGCTTCAATCTCCAAGGTACTCTCCAGCAACACAGGTA 606
QY 241 TTCTCAAGATCACCAGTGTGGACACTCGAGTACTGCGACATACATCTACTGTCTCGAAG- 299
Db 607 TTCTCAAGATCACCAGTGTGGACACTCGAGTACTGCGACATACATCTACTGTCTCGAAGA 666
QY 300 -----GGTCTCTTAAGTGGGGGGACTATGCTATGGACTCTGGGGTCAAGGAACCTCAGTC 351
Db 667 AGTCTCTATGTAATGGGGGGGGACTATGCTATGGACTCTGGGGTCAAGGAACCTCAGTC 726
QY 352 ACCGTCTCTCTCA 363
Db 727 ACCGTCTCTCTCA 738

RESULT 6
PCT-US95-07372-9
; Sequence 9, Application PC/TUS9507372
; GENERAL INFORMATION:
; APPLICANT: Oklahoma Medical Research Foundation
; TITLE OF INVENTION: Calcium Binding Recombinant
; TITLE OF INVENTION: Antibody Against Protein C
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07372
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMRF106CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: HPC-4 Heavy Chain Variable Region (VH Gamma)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..57
; OTHER INFORMATION: /note= "Signal peptide encoded by
; OTHER INFORMATION: nucleotides 1 through 57."

FEATURE:
NAME/KEY: misc feature
LOCATION: 58, 417
OTHER INFORMATION: /note= "Mature peptide encoded by
OTHER INFORMATION: nucleotides 58 through 417."
PCT-US95-07372-9

Query Match 81.7%; Score 296.4; DB 5; Length 417;
Best Local Similarity 90.6%; Pred. No. 5.1e-93;
Matches 328; Conservative 0; Mismatches 31; Indels 3; Gaps 1;

QY 1 CAGGTACTCTGAAGAGTCTGCGCTGGATATTCAGCCCTCCAGACCCCTCAGTCTG 60
DB 58 CAGGTACTCTGAAGAGTCTGCGCTGGATATTCAGCCCTCCAGACCCCTCAGTCTG 117
QY 61 ACTTGTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
DB 118 ACTTGTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 177
QY 121 CAGCCTTCAGAAAGGCTCTGGAGTCTGGAGTCTGGAGTCTGGAGTCTGGAGTCTGG 180
DB 178 CAGCCTTCAGAAAGGCTCTGGAGTCTGGAGTCTGGAGTCTGGAGTCTGGAGTCTGG 237
QY 181 TATAACCCATCCCTGAAGAGCCGGCTTACAACTCCAGGATACCTCCAGCAACAGGTA 240
DB 238 TATAACCCATCCCTGAAGAGCCGGCTTACAACTCCAGGATACCTCCAGCAACAGGTA 297
QY 241 TTCCTCAAGATCACCAAGTCTGGAGTCTGGAGTCTGGAGTCTGGAGTCTGGAGTCTGG 300
DB 298 TTCCTCAAGATCACCAAGTCTGGAGTCTGGAGTCTGGAGTCTGGAGTCTGGAGTCTGG 357
QY 301 GTCTCTCTAACTCCCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTAT 360
DB 358 ATGGAT---GATTACGACGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTAT 414
QY 361 TC 362
DB 415 TC 416

RESULT 7
US-08-553-501A-28
Sequence 28, Application US/08553501A
Patent No. 5856135
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,501A
FILING DATE: 20-FEB-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/00859
FILING DATE: 30-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-129787
FILING DATE: 31-MAY-1993

ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/177/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 418 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..417
FEATURE:
NAME/KEY: mat peptide
LOCATION: 1..417
US-08-553-501A-28

Query Match 80.2%; Score 291; DB 2; Length 418;
Best Local Similarity 89.5%; Pred. No. 3.8e-91;
Matches 325; Conservative 0; Mismatches 35; Indels 3; Gaps 1;

QY 1 CAGGTACTCTGAAGAGTCTGCGCTGGATATTCAGCCCTCCAGACCCCTCAGTCTG 60
DB 58 CAGGTACTCTGAAGAGTCTGCGCTGGATATTCAGCCCTCCAGACCCCTCAGTCTG 117
QY 61 ACTTGTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
DB 118 ACTTGTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 177
QY 121 CAGCCTTCAGAAAGGCTCTGGAGTCTGGAGTCTGGAGTCTGGAGTCTGGAGTCTGG 180
DB 178 CAGCCTTCAGAAAGGCTCTGGAGTCTGGAGTCTGGAGTCTGGAGTCTGGAGTCTGG 237
QY 181 TATAACCCATCCCTGAAGAGCCGGCTTACAACTCCAGGATACCTCCAGCAACAGGTA 240
DB 238 TATAACCCATCCCTGAAGAGCCGGCTTACAACTCCAGGATACCTCCAGCAACAGGTA 297
QY 241 TTCCTCAAGATCACCAAGTCTGGAGTCTGGAGTCTGGAGTCTGGAGTCTGGAGTCTGG 300
DB 298 TTCCTCAAGATCACCAAGTCTGGAGTCTGGAGTCTGGAGTCTGGAGTCTGGAGTCTGG 357
QY 301 GTCTCTCTAACTCCCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTAT 360
DB 358 GAGGAT---TACGACGAAGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTAT 414
QY 361 TCA 363
DB 415 TCA 417

RESULT 8
US-09-205-231-28
Sequence 28, Application US/09205231
Patent No. 6121423
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: HIRATA, Yuichi
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/205,231
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA: US/08/553,501
FILING DATE: 20-FEB-1996
APPLICATION NUMBER: WO PCT/JP94/00859
FILING DATE: 30-MAY-1994
PRIORITY APPLICATION DATA: JP 5-129787
FILING DATE: 31-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/177/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 418 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..417
FEATURE:
NAME/KEY: mat peptide
LOCATION: 1..417
US-09-205-231-28

Query Match 80.2%; Score 291; DB 3; Length 418;
Best Local Similarity 89.5%; Pred. No. 3.8e-91;
Matches 325; Conservative 0; Mismatches 35; Indels 3; Gaps 1;
QY 1 CAGGTACTCTGAAGAGTCTGGCCCTGGGATATTGCGCCCTCCAGACCCCTCAGTCTG 60
DB 58 CAGGTACTCTGAAGAGTCTGGCCCTGGGATATTGCGCCCTCCAGACCCCTCAGTCTG 117
QY 61 ACTTGTTCTTTCTCTGGTCTTCTGAGCACTTCTGGTATGGGTGTGAGCTGGATTGGA 120
DB 118 ACTTGTTCTTTCTCTGGTCTTCTGAGCACTTCTGGTATGACCGTGGATTGCT 177
QY 121 CAGCCTTCAGAAAGGCTCTGGAGTGGCTGGGACACATTTACTGGGATGATGACAGCGC 180
DB 178 CAGCCTTCAGAAAGGCTCTGGAGTGGCTGGGACACATTTGGTGAATGATGATAGTAC 237
QY 181 TATAACCCATCCCTGAAGAGCGGCTTACAACTCTCAAGGATACCTCCAGCAACAGGTA 240
DB 238 TATAACCCAGCCTGAAGAGCGGCTCACAATCTCAAGGATACCTCCAGCAACAGGTA 297
QY 241 TTCTCTAAGATCAACGATGGGACCTCGAGATCTGCGCACATCTACTGTGTGCGAAGG 300
DB 298 TTCTCTAAGATCGCAGTGTGGTCACTGCGAGATCTGCGCACATCTACTGTGTGCGAAGG 357
QY 301 GTCTCTTAAGTCTATGATGAGTCTGAGTCTGAGGTCAGGAAACCTCAGTCAACGCTCTCC 360
DB 358 GAGGAT---TACGACGAGATGAGTACTTGGGTCAAGGAAACCTCAGTCAACGCTCTCC 414
QY 361 TCA 363
DB 415 TCA 417

RESULT 9

US-08-436-463-1
Sequence 1, Application US/08436463
Patent No. 5760185
GENERAL INFORMATION:
APPLICANT: KIMACHI, Kazuhiko
APPLICANT: MAEDA, Hiroaki
APPLICANT: NISHIYAMA, Kiyoto
APPLICANT: TOKIYOSHI, Sachio
TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,463
FILING DATE: 26-JUN-1995
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 341255/1992
FILING DATE: 28-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: KIMACHI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 462 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 21..449
US-08-436-463-1

Query Match 72.1%; Score 261.8; DB 1; Length 462;
Best Local Similarity 92.6%; Pred. No. 5.3e-81;
Matches 275; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 1 CAGGTACTCTGAAGAGTCTGGCCCTGGGATATTGCGCCCTCCAGACCCCTCAGTCTG 60
DB 78 CAGGTACTCTGAAGAGTCTGGCCCTGGGATATTGCGCCCTCCAGACCCCTCAGTCTG 137
QY 61 ACTTGTTCTTTCTCTGGTCTTCTGAGCACTTCTGGTATGGGTGTGAGCTGGATTGGA 120
DB 138 ACTTGTTCTTTCTCTGGTCTTCTGAGCACTTCTGGTATGGGTGTGAGCTGGATTGCT 197
QY 121 CAGCCTTCAGAAAGGCTCTGGAGTGGCTGGGACACATTTACTGGGATGATGACAGCGC 180
DB 198 CAGCCTTCAGAAAGGCTCTGGAGTGGCTGGGACACATTTGGTGGGATGATGTCAGCGC 257
QY 181 TATAACCCATCCCTGAAGAGCGGCTTACAACTCTCAAGGATACCTCCAGCAACAGGTA 240
DB 258 TATAACCCAGCCTTCAGAGCGGCTGACTATCTTCCAGGATACCTCCAGCAGCAGGTA 317
QY 241 TTCTCTCAAGATCACCAGTGTGGACACTCGAGATACTGCCACATACTACTGTGTCTGGA 297
DB 318 TTCTCTCAAGATCGCCAGCGTGGACACTGCAGATACTGCCACATATTTTGTGTCTGGA 374

RESULT 10
US-08-408-133-1
; Sequence 1, Application US/08408133
; Patent No. 5750078
; GENERAL INFORMATION:
; APPLICANT: SHITARA, Kenya
; APPLICANT: HANAI, No. 5750078uo
; APPLICANT: HASEGAWA, Mamoru
; APPLICANT: MIYAJI, Hirohisa
; APPLICANT: KUWANA, Yoshinisa
; TITLE OF INVENTION: Process for Producing Humanized Chimera
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vandertye, P.C.
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/408,133
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/292,178
; FILING DATE:
; APPLICATION NUMBER: US 07/947,674
; FILING DATE: 17-SEPT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAWFORD, Arthur R
; TELEPHONE: (703)816-4000
; TELEFAX: (803)816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 812 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ORIGINAL SOURCE:
; STRAIN: Hybridoma KM50
; FEATURE:
; NAME/KEY: TATA signal
; LOCATION: 256..262
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: mat peptide
; LOCATION: 441..806
; OTHER INFORMATION: /product= "RAT IMMUNOGLOBULIN HEAVY
; OTHER INFORMATION: CHAIN VARIABLE REGION"
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 300..440
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(300..345, 429..806)
; OTHER INFORMATION:
US-08-408-133-1
Query Match 69.1%; Score 250.8; DB 1; Length 812;
Best Local Similarity 82.2%; Pred. No. 4.6e-77;
Matches 301; Conservative 0; Mismatches 62; Indels 3; Gaps 1;

QY 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGAGCCCTCCAGAGCCCTCAGTCTG 60
Db 441 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGAGCCCTCCAGAGCCCTCAGTCTG 500
QY 61 ACTTGTCTCTTCTCTGGGTTTTCACCTGAGCACCTTCTGGTATGGGTGTGAGCTGGATTGGA 120
Db 501 ACTTGTCTCTTCTCTGGGTTTTCACCTGAGCACCTTCTGGTATGGGTGTGAGCTGGATTGGA 560
QY 121 CAGCCTTCAGGAAGGCTCTGGAGTGGCTGGGACACATTTACTTGGGATGATGACAGCCG 180
Db 561 CAGCCTTCAGGAAGGCTCTGGAGTGGCTGGGACACATTTACTTGGGATGATGATGATGATGATG 620
QY 181 TATAACCCATCCCTGGAAGAGCCGCTTACAACTCTCAAGGATACCTCCAGCAACACAGGTA 240
Db 621 TAGCATCCATCTCTGAAACACCGCTCACAACTCTCAAGGACACCTCCACACACAGCA 680
QY 241 TTCCTCAAGATCAGAGTGTGGACATCTGAGATATGCGCATATCTACTGTGTCGAAGG 300
Db 681 TTCCTCAAGATCAGCAATATGAGACATCTGAGATATGCGCATATCTACTGTGTCGAAGG 740
QY 301 GTCTCTCTAACTGCTATGCTA---TGGACTACTGGGTCAGGAACTCAGTCACCGTC 357
Db 741 GGGCTACGGAGGTATAGTACGCTTTGATTGCGGCGCACCGAGTCTATGTCACAGTC 800
QY 358 TCCTCA 363
Db 801 TCCTCA 806

RESULT 11
US-08-454-683-1
; Sequence 1, Application US/08454683
; Patent No. 5807548
; GENERAL INFORMATION:
; APPLICANT: SHITARA, Kenya
; APPLICANT: HANAI, No. 5807548uo
; APPLICANT: HASEGAWA, Mamoru
; APPLICANT: MIYAJI, Hirohisa
; APPLICANT: KUWANA, Yoshinisa
; TITLE OF INVENTION: Process for Producing Humanized Chimera
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vandertye, P.C.
; STREET: No. 5807548th Glebe Road
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,683
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/408,133
; FILING DATE:
; APPLICATION NUMBER: US 08/292,178
; FILING DATE:
; APPLICATION NUMBER: US 07/947,674
; FILING DATE: 17-SEPT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAWFORD, Arthur R
; TELEPHONE: (703)816-4000
; TELEFAX: (803)816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 812 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ORIGINAL SOURCE:
; STRAIN: Hybridoma KM50
; FEATURE:
; NAME/KEY: TATA signal
; LOCATION: 256..262
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: mat peptide
; LOCATION: 441..806
; OTHER INFORMATION: /product= "RAT IMMUNOGLOBULIN HEAVY
; OTHER INFORMATION: CHAIN VARIABLE REGION"
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 300..440
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(300..345, 429..806)
; OTHER INFORMATION:
US-08-408-133-1
Query Match 69.1%; Score 250.8; DB 1; Length 812;
Best Local Similarity 82.2%; Pred. No. 4.6e-77;
Matches 301; Conservative 0; Mismatches 62; Indels 3; Gaps 1;

SEQUENCE CHARACTERISTICS:
LENGTH: 812 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ORIGINAL SOURCE:
STRAIN: Hybridoma KM50
FEATURE:
NAME/KEY: TATA signal
LOCATION: 256..262
OTHER INFORMATION:
FEATURE:
NAME/KEY: mat peptide
LOCATION: 441..806
OTHER INFORMATION: /product= 'RAT IMMUNOGLOBULIN HEAVY
OTHER INFORMATION: CHAIN VARIABLE REGION'
FEATURE:
NAME/KEY: sig peptide
LOCATION: 300..440
OTHER INFORMATION:
FEATURE:
NAME/KEY: CDS
LOCATION: join(300..345, 429..806)
OTHER INFORMATION:
US-08-454-683-1

Query Match 69.1%; Score 250.8; DB 1; Length 812;
Best Local Similarity 82.2%; Pred. No. 4.6e-77;
Matches 301; Conservative 0; Mismatches 62; Indels 3; Gaps 1;
QY 1 CAGGTTACTCTCAAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGTCTG 60
DB 441 CAGGTTACTCTCAAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGTCTG 500
QY 61 ACTTGTTCTTTCTCTGGGTTTCTCAGTACGACTTCTGATGGTGTGAGTGGATTGGA 120
DB 501 ACTTGTTCTTTCTCTGGGTTTCTCAGTACGACTTCTGATGGTGTGAGTGGATTGGA 560
QY 121 CAGCCTTCAGGAAGGGTCTGGAGTGGCTGGCACATTTACTGGGATGATGACAGCGC 180
DB 561 CAGTCTTCAGGAAGGGTCTGGAGTGGCTGGCACATTTACTGGGATGATGACAGCGC 620
QY 181 TATAACCCATCCTGAGAGCCGGCTTACAATCTCCAGGATACCTCCAGCAACCGAGTA 240
DB 621 TACAATCCATCTCTGAAACACCGCTCAAAATCTCCAGGACACCTCCCAACCAACGCA 680
QY 241 TTCTCTCAAGATCACCAGTCTGGACACTCGGATGCTGCGACATTTACTGGGATGATGACAGCGC 300
DB 681 TTCTCTCAAGATCACCAGTCTGGACACTCGGATGCTGCGACATTTACTGGGATGATGACAGCGC 740
QY 301 GTCTCTCTAACTGCTATGCTA---TGGACTACTGGGGTCAAGGAACCTCAGTCAACCGTC 357
DB 741 GGGGCTACGAGGGTATAGTGGCTTTGATTACTGGGGCCACGGAGTCATGCTCAGATC 800
QY 358 TCCTCA 363
DB 801 TCCTCA 806

RESULT 12
US-08-116-778E-16
Sequence 16, Application US/08116778E
Patent No. 5830470
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KUWANA, YOSHITHISA
APPLICANT: HASEGAWA, MANORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES

NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHUYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/116,778E
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-59
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 812 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: HYBRIDOMA KM50
FEATURE:
NAME/KEY: TATA signal
LOCATION: 261..267
US-08-116-778E-16

Query Match 69.1%; Score 250.8; DB 2; Length 812;
Best Local Similarity 82.2%; Pred. No. 4.6e-77;
Matches 301; Conservative 0; Mismatches 62; Indels 3; Gaps 1;
QY 1 CAGGTTACTCTCAAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGTCTG 60
DB 441 CAGGTTACTCTCAAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGTCTG 500
QY 61 ACTTGTTCTTTCTCTGGGTTTCTCAGTACGACTTCTGATGGTGTGAGTGGATTGGA 120
DB 501 ACTTGTTCTTTCTCTGGGTTTCTCAGTACGACTTCTGATGGTGTGAGTGGATTGGA 560
QY 121 CAGCCTTCAGGAAGGGTCTGGAGTGGCTGGCACATTTACTGGGATGATGACAGCGC 180
DB 561 CAGTCTTCAGGAAGGGTCTGGAGTGGCTGGCACATTTACTGGGATGATGACAGCGC 620
QY 181 TATAACCCATCCTGAGAGCCGGCTTACAATCTCCAGGATACCTCCAGCAACCGAGTA 240
DB 621 TACAATCCATCTCTGAAACACCGCTCAAAATCTCCAGGACACCTCCCAACCAACGCA 680
QY 241 TTCTCTCAAGATCACCAGTCTGGACACTCGGATGCTGCGACATTTACTGGGATGATGACAGCGC 300
DB 681 TTCTCTCAAGATCACCAGTCTGGACACTCGGATGCTGCGACATTTACTGGGATGATGACAGCGC 740
QY 301 GTCTCTCTAACTGCTATGCTA---TGGACTACTGGGGTCAAGGAACCTCAGTCAACCGTC 357
DB 741 GGGGCTACGAGGGTATAGTGGCTTTGATTACTGGGGCCACGGAGTCATGCTCAGATC 800
QY 358 TCCTCA 363
DB 801 TCCTCA 806

RESULT 13
US-08-454-680-1

Sequence 1, Application US/08454680
Patent No. 5866692
GENERAL INFORMATION:
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUWANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA
TITLE OF INVENTION: ANTIBODY
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,680
FILING DATE: 31-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/408,133
FILING DATE: 21-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,178
FILING DATE: 17-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/947,674
FILING DATE: 17-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-238375
FILING DATE: 18-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 249-74
TELEPHONE: 7038164000
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 812 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: TATA_signal
LOCATION: 256..262
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 441..806
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 300..440
FEATURE:
NAME/KEY: CDS
LOCATION: join(300..345, 430..806)
US-08-454-680-1
Query Match 69.1%; Score 250.8; DB 2; Length 812;
Best Local Similarity 82.2%; Pred. No. 4.6e-77;
Matches 301; Conservative 0; Mismatches 62; Indels 3; Gaps 1;
1 CAGGTACTCTGAAGAGTCTGGGATATTCAGCCCTCCAGACCCCTCAGTCTG 60
|||||

Db 441 CAGGTACTCTGAAGAGTCTGGGATATTCAGCCCTCCAGACCCCTCAGTCTG 500
QY 61 ACTTGTCTCTCTCTGGTCTTCTGAGCAGTCTTCTGGTATGGGTGAGTGGATTGGA 120
DB 501 ACTTGTCTCTCTCTGGTCTTCTGAGCAGTCTTCTGGTATGGGTGAGTGGATTGCGT 560
QY 121 CAGCCTTCAGGAAAGGGTCTGGAGTGGTGGCAGACATTTACTGGGATGATGACAAGGCG 180
DB 561 CAGTCTTCAGGAAAGGGTCTGGAGTGGTGGCAGACATTTACTGGGATGATGACTAAGTAC 620
QY 181 TATAACCCATCCCTGAAGAGCGGCTTACATCTCCAAAGGATACCTCCAGCAACAGGTA 240
DB 621 TACAATCCATCTCTGAAGAAACCGGCTCACAACTCTCCAAGGACACCTCCAAACCAAGCA 680
QY 241 TTCCTCAAGATCACAGTGTGGACACTCGAGATATCGCAGATATCTCCATATCTACTGTGCTGGAAGG 300
DB 681 TTCCTCAAGATCACCAATATGGACACTCGCAGATATCTCCATATCTACTGTGCTGGGAGA 740
QY 301 GTCTCTTAAGTGCCTATGCTA---TGGACTACTGGGGTCAAGGAACCTCAGTCAACGCTC 357
DB 741 GGGGCTACGGAGGGTATAGTGAGCTTTGATTACTGGGGCCACGGAGTCATGGTCAAGTC 800
QY 358 TCCTCA 363
DB 801 TCCTCA 806

RESULT 14
US-08-438-562-16
Sequence 16, Application US/08438562
Patent No. 5874255
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KUWANA, YOSHIHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,562
FILING DATE: 10-MAY-95
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/116,778
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-76
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 812 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 812 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
STRAIN: HYBRIDOMA KM50
FEATURE:
NAME/KEY: TATA signal
LOCATION: 261..267
US-08-438-562-16

Query Match 69.1%; Score 250.8; DB 2; Length 812;
Best Local Similarity 82.2%; Pred. No. 4.6e-77;
Matches 301; Conservative 0; Mismatches 62; Indels 3; Gaps 1;

QY 1 CAGGTTACTCTGAAAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGTCTG 60
DB 441 CAGGTTACTCTGAAAGAAATCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGTCTG 500
QY 61 ACTTGTCTCTTCTCTGGGTTTTCACCTGAGCACCTTCTGGTATGGGTGTGAGCTGGATTGGA 120
DB 501 ACTTGTCTCTTCTCTGGGTTTTCACCTGAGCACCTTATGGTATGGTGTGAGCTGGATTGGA 560
QY 121 CAGCCTTCAGGAAAGGCTCTGGAGTGGCTGGCACACATTTACTGGGATGATGACACGCG 180
DB 561 CAGTCTTCAGGAAAGGCTCTGGAGTGGCTGGCACACATTTACTGGGATGATGACACGCG 620
QY 181 TATAACCCATCCCTGAGAGCCGGCTTACAATCTCCAAGGATACCTCCAGCAACCCAGGTA 240
DB 621 TACATTCATCTCTGAAAACCGGCTCACATCTCCAGGACACCTCCACCAACCAAGCA 680
QY 241 TTCTCAAGATCACCAGTGTGGACACTCGAGATATCGCCACATATCTACTGTCTCGAAG 300
DB 681 TTCTCAAGATCACCAGTGTGGACACTCGAGATATCGCCACATATCTACTGTCTCGAAG 740
QY 301 GTCTCTTAAGTCTGCTATGCTA---TGGACTCTGGGGTCAAGGAACCTCAGTCAACGTC 357
DB 741 GGGGCTACGGAGGGTATAGTACGCTTTGATTCTGGGGCCACGGAGTCATGGTCAAGTC 800

Search completed: January 14, 2004, 17:48:16
Job time : 47 secs

MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: HYBRIDOMA KM50
FEATURE:
NAME/KEY: TATA signal
LOCATION: 261..267
US-08-438-562-16

Query Match 69.1%; Score 250.8; DB 2; Length 812;
Best Local Similarity 82.2%; Pred. No. 4.6e-77;
Matches 301; Conservative 0; Mismatches 62; Indels 3; Gaps 1;

QY 1 CAGGTTACTCTGAAAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGTCTG 60
DB 441 CAGGTTACTCTGAAAGAAATCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGTCTG 500
QY 61 ACTTGTCTCTTCTCTGGGTTTTCACCTGAGCACCTTCTGGTATGGGTGTGAGCTGGATTGGA 120
DB 501 ACTTGTCTCTTCTCTGGGTTTTCACCTGAGCACCTTATGGTATGGTGTGAGCTGGATTGGA 560
QY 121 CAGCCTTCAGGAAAGGCTCTGGAGTGGCTGGCACACATTTACTGGGATGATGACACGCG 180
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QY 181 TATAACCCATCCCTGAGAGCCGGCTTACAATCTCCAAGGATACCTCCAGCAACCCAGGTA 240
DB 621 TACATTCATCTCTGAAAACCGGCTCACATCTCCAGGACACCTCCACCAACCAAGCA 680
QY 241 TTCTCAAGATCACCAGTGTGGACACTCGAGATATCGCCACATATCTACTGTCTCGAAG 300
DB 681 TTCTCAAGATCACCAGTGTGGACACTCGAGATATCGCCACATATCTACTGTCTCGAAG 740
QY 301 GTCTCTTAAGTCTGCTATGCTA---TGGACTCTGGGGTCAAGGAACCTCAGTCAACGTC 357
DB 741 GGGGCTACGGAGGGTATAGTACGCTTTGATTCTGGGGCCACGGAGTCATGGTCAAGTC 800

RESULT 15
US-08-483-528B-16
Sequence 16, Application US/08483528B
Patent No. 593532
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KUWANA, YOSHIOHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHUYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,528B
FILING DATE: 07-JUN-95
CLASSIFICATION: 536
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100

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OM nucleic - nucleic search, using sw model

Run on: January 14, 2004, 16:03:20 ; Search time 215.81 Seconds
(without alignments)
5928.789 Million cell updates/sec

Title: US-09-759-112A-5

Perfect score: 363

Sequence: 1 caggttactctgaagagtc.....ctcagtcaccgtctctccta 363

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2324096 seqs, 1762381658 residues

Total number of hits satisfying chosen parameters: 4648192

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	363	100.0	363	11	US-09-759-112A-6
3	313.4	86.3	483	10	US-09-879-461-3
4	311.8	85.9	423	10	US-09-879-461-9
5	311.8	85.9	426	13	US-10-010-942B-15
6	299	82.4	369	11	US-09-995-529-11
7	284.4	78.3	465	7	US-09-881-823-7
8	270.8	74.6	357	12	US-10-323-903-4
9	250.8	69.1	812	9	US-09-784-304-1
10	250.8	69.1	812	13	US-10-166-626-1
11	250.8	69.1	812	15	US-10-195-752-16
12	250.8	69.1	812	15	US-10-265-713-1
13	191.4	52.7	423	13	US-10-255-478-50
14	183	50.4	759	13	US-10-072-301-22
15	183	50.4	759	13	US-10-072-301-30

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16 183 50.4 759 13 US-10-071-866-22 Sequence 22, Appl
17 183 50.4 759 13 US-10-071-866-30 Sequence 30, Appl
18 183 50.4 759 13 US-10-360-828-22 Sequence 22, Appl
19 183 50.4 759 13 US-10-360-828-30 Sequence 20, Appl
20 182.6 50.3 1625 12 US-10-108-260A-2241 Sequence 2241, Ap
21 180.4 49.7 1557 13 US-10-225-108A-9 Sequence 9, Appl
22 179.2 49.4 288 11 US-09-995-529-15 Sequence 15, Appl
23 178.6 49.2 666 11 US-09-972-656-69 Sequence 69, Appl
24 173.4 47.8 759 13 US-10-072-301-16 Sequence 16, Appl
25 173.4 47.8 759 13 US-10-071-866-16 Sequence 16, Appl
26 173.4 47.8 759 13 US-10-360-828-16 Sequence 16, Appl
27 172 47.4 684 11 US-09-972-656-83 Sequence 83, Appl
28 171.8 47.3 759 13 US-10-072-301-24 Sequence 24, Appl
29 171.8 47.3 759 13 US-10-071-866-24 Sequence 24, Appl
30 171.8 47.3 759 13 US-10-360-828-24 Sequence 24, Appl
31 171 47.1 423 10 US-09-879-461-11 Sequence 11, Appl
32 168.4 46.4 646 10 US-09-736-457-1113 Sequence 1113, Ap
33 168.4 46.4 646 10 US-09-902-941-1113 Sequence 1113, Ap
34 168.4 46.4 646 10 US-09-849-626-1113 Sequence 1113, Ap
35 168.4 46.4 646 13 US-10-113-872-1113 Sequence 1113, Ap
36 168.4 46.4 646 15 US-10-017-754-1113 Sequence 1113, Ap
37 165 45.5 714 8 US-08-940-544-4 Sequence 4, Appl
38 165 45.5 714 13 US-10-075-947A-2 Sequence 2, Appl
39 165 45.5 1173 13 US-10-075-947A-4 Sequence 4, Appl
40 163.2 45.0 378 9 US-09-740-002-15 Sequence 15, Appl
41 163.2 45.0 378 12 US-10-384-356-15 Sequence 15, Appl
42 163.2 45.0 1428 9 US-09-740-002-19 Sequence 19, Appl
43 163.2 45.0 1428 12 US-10-384-356-19 Sequence 19, Appl
44 162 44.6 1446 13 US-10-409-938-22 Sequence 22, Appl
45 160.2 44.1 454 10 US-09-797-941A-1 Sequence 1, Appl

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ALIGNMENTS

RESULT 1

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US-09-759-112A-5
; Sequence 5, Application US/09759112A
; Publication No. US20030100741A1
; GENERAL INFORMATION:
; APPLICANT: Mueller, Sybille
; APPLICANT: Kohler, Heinz
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING VARIABLE REGIONS OF HEAVY AND LIGHT
; TITLE OF INVENTION: OF MONOCLONAL ANTIBODY 1P7, AN ANTI-IDIOTYPIC ANTIBODY REACTIVE
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 200-013
; CURRENT APPLICATION NUMBER: US/09/759,112A
; CURRENT FILING DATE: 2001-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 363
; TYPE: DNA
; ORGANISM: mouse
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(362)
; OTHER INFORMATION: 1P7 VH chain gene
US-09-759-112A-5

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Query Match      100.0%; Score 363; DB 11; Length 363;
Best Local Similarity 100.0%; Pred. No. 1.5e-114;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CAGGTACTCTGAAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGTCTG 60
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Db 1 CAGGTACTCTGAAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGTCTG 60
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QY 61 ACTTGTTCTTTCTCGGGTCTTTTCTACTGAGCACTTCTGATGGGTGAGTGTGATTCGA 120
   |||
Db 61 ACTTGTTCTTTCTCGGGTCTTTTCTACTGAGCACTTCTGATGGGTGAGTGTGATTCGA 120
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QY 121 CAGCCTTCAGGAGGGTCTGGAGTGGCTGGCGACACATTTTACTGGGATGATGACAGCGC 180

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Db 121 CAGCCTTCAGGAAGGCTCGAGTGGCTGGGACACATTTACTGGGATGATGACAGCGC 180
Qy 181 TATAACCCATCCCTGAAGAGCGGCTTCAATCTCAAGATACCTCCAGCAACAGGTA 240
Db 181 TATAACCCATCCCTGAAGAGCGGCTTCAATCTCAAGATACCTCCAGCAACAGGTA 240
Qy 241 TTCCTCAAGATCACCAGTGTGGACACTCGAGATACCTGCCACATACCTACTGTGCTCGAAGG 300
Db 241 TTCCTCAAGATCACCAGTGTGGACACTCGAGATACCTGCCACATACCTACTGTGCTCGAAGG 300
Qy 301 GTCTCTTAAGTCCCTATGGAAGTCTGGGTCAAGGAACCTCAGTCAACCTCTCC 360
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Qy 361 TCA 363
Db 361 TCA 363

RESULT 2
US-09-759-112a-6
; Sequence 6, Application US/09759112a
; Publication No. US20030100741A1
; GENERAL INFORMATION:
; APPLICANT: Mueller, Sybille
; APPLICANT: Kohler, Heinz
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING VARIABLE REGIONS OF HEAVY AND LIGHT
; TITLE OF INVENTION: OF MONOCLONAL ANTIBODY 1P7, AN ANTI-IDIOTYPIC ANTIBODY REACTIVE
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 200-013
; CURRENT APPLICATION NUMBER: US/09/759,112a
; CURRENT FILING DATE: 2001-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 363
; TYPE: DNA
; ORGANISM: mouse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(363)
; OTHER INFORMATION: 1P7 VH chain gene
US-09-759-112a-6

Query Match 100.0%; Score 363; DB 11; Length 363;
Best Local Similarity 100.0%; Pred. No. 1.5e-114;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 ACTTGTCTTTCTCTGGGTTTCACTGAGCACTTCTGGTATGGGTGAGCTGGATTGGA 120
Qy 121 CAGCCTTCAGGAAGGCTCGAGTGGCTGGACACATTTACTGGGATGATGACAGCGC 180
Db 121 CAGCCTTCAGGAAGGCTCGAGTGGCTGGACACATTTACTGGGATGATGACAGCGC 180
Qy 181 TATAACCCATCCCTGAAGAGCGGCTTACAATCTCAAGATACCTCCAGCAACAGGTA 240
Db 181 TATAACCCATCCCTGAAGAGCGGCTTACAATCTCAAGATACCTCCAGCAACAGGTA 240
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Db 241 TTCCTCAAGATCACCAGTGTGGACACTCGAGATACCTGCCACATACCTACTGTGCTCGAAGG 300
Qy 301 GTCTCTTAAGTCCCTATGGAAGTCTGGGTCAAGGAACCTCAGTCAACCTCTCC 360
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Qy 361 TCA 363
Db 361 TCA 363

RESULT 3
US-09-879-461-3
; Sequence 3, Application US/09879461
; Publication No. US20020193575A1
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; Gross, Mitchell S.
; Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: Corporate Intellectual Property, UW2220 - 709
; Swedeland Rd.
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/879,461
; FILING DATE: 12-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/612,929
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/136,783
; FILING DATE: 14-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 483 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 64..483
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-879-461-3

Query Match 86.3%; Score 313.4; DB 10; Length 483;
Best Local Similarity 91.5%; Pred. No. 2e-97;
Matches 332; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTCAGGCCCTCCAGACCCCTCAGTCTG 60
Db 121 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTCAGGCCCTCCAGACCCCTCAGTCTG 180
Qy 61 ACTTGTCTTTCTCTGGGTTTCACTGAGCACTTCTGGTATGGGTGAGCTGGATTGGA 120
Db 181 ACTTGTCTTTCTCTGGGTTTCACTGAGCACTTCTGGTATGGGTGAGCTGGATTGGA 240
Qy 121 CAGCCTTCAGGAAGGCTCGAGTGGCTGGACACATTTACTGGGATGATGACAGCGC 180
Db 241 CAGCCTTCAGGAAGGCTCGAGTGGCTGGACACATTTACTGGGATGATGACAGCGC 300

181 TATAAACCCTCCCTGAAGAGCGGCTTACAACTCTCAAGGATACCTCCAGCAACAGGTA 240
 301 TATAAACCCTCCCTGAAGAGCGGCTTACAACTCTCAAGGATACCTCCAGCAACAGGTA 360
 241 TTCTCAAGATCAACAGTGTGGACACTCGAGATGTCACATATCTACTGTGTGTCGAAGG 300
 361 TTCTCAAGATCAACAGTGTGGACACTCGAGATGTCACATATCTACTGTGTGTCGAAGG 420
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 421 GAGACTGTGTTCTACTGGTACTTCGATGTCGGGGCGCAGGACCAAGTACCGTCTCC 480
 361 TCA 363
 481 TCA 483

RESULT 4

US-09-879-461-9
 ; Sequence 9, Application US/09879461
 ; Publication No. US20020193575A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Holmes, Stephen D.
 ; Gross, Mitchell S.
 ; Sylvester, Daniel R.
 ; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
 ; Treatment of IL4 Mediated Disorders
 ; NUMBER OF SEQUENCES: 58
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SmithKline Beecham Corporation
 ; STREET: Corporate Intellectual Property, UW2220 - 709
 ; CITY: King of Prussia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19406-2799
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/879,461
 ; FILING DATE: 12-Jun-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/612,929
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: US 08/136,783
 ; FILING DATE: 14-OCT-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sutton, Jeffrey A.
 ; REGISTRATION NUMBER: 34,028
 ; REFERENCE/DOCKET NUMBER: P50186-2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (215) 270-5024
 ; TELEFAX: (215) 270-5090
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 423 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1..423
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-879-461-9

Query Match 85.9%; Score 311.8; DB 10; Length 423;
 Best Local Similarity 91.2%; Pred. No. 6.9e-97;

Matches 331; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
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 QY 61 CAGGTTACTCTGAAAGAGTCTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCAGTCTG 120
 Db |||||
 QY 61 ACTTGTCTTTCTCTGGGTTTTCACCTGAGCACCTTCTGGTATGGGTGTGAGTGTGATTCGA 120
 Db |||||
 QY 121 ACTTGTCTTTCTCTGGGTTTTCACCTGAGCACCTTCTGGTATGGGTGTGAGTGTGATTCGT 180
 Db |||||
 QY 121 CAGCCTTTCAAGAAAGGCTCTGGAGTGGCTGGCACACATTTACTGGGATGATGACAAGGC 180
 Db |||||
 QY 181 CAGCCTTTCAAGAAAGGCTCTGGAGTGGCTGGCACACATTTACTGGGATGATGACAAGGC 240
 Db |||||
 QY 181 TATAACCCATCCCTGAAGAGCGGCTTACAACTCTCAAGGATACCTCCAGCAACAGGTA 240
 Db |||||
 QY 241 TATAACCCATCCCTGAAGAGCGGCTTACAACTCTCAAGGATACCTCCAGCAACAGGTA 300
 Db |||||
 QY 241 TTCTCAAGATCAACAGTGTGGACACTCGAGATGTCACATATCTACTGTGTGTCGAAGG 300
 Db |||||
 QY 301 TTCTCAAGATCAACAGTGTGGACACTCGAGATGTCACATATCTACTGTGTGTCGAAGG 360
 Db |||||
 QY 301 GTCTCTTAACTGCTATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCC 360
 Db |||||
 QY 361 GAGACTGTGTTCTACTGGTACTTCGATGTCGGGGCGCAGGACCAAGTACCGTCTCC 420
 Db |||||
 QY 361 TCA 363
 421 TCA 423

RESULT 5

US-10-010-942B-15
 ; Sequence 15, Application US/10010942B
 ; Publication No. US20030165496A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Basi, Guriq
 ; APPLICANT: Saidanba, Jose
 ; APPLICANT: Yednock, Ted
 ; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
 ; FILE REFERENCE: BETA AMYLOID PEPTIDE
 ; CURRENT APPLICATION NUMBER: US/10/010,942B
 ; CURRENT FILING DATE: 2002-12-06
 ; PRIOR FILING DATE: 2000-12-06
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 15
 ; LENGTH: 426
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(426)
 ; FEATURE:
 ; NAME/KEY: sig_peptide
 ; LOCATION: (1)...(57)
 ; US-10-010-942B-15

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 Best Local Similarity 92.4%; Pred. No. 6.9e-97;
 Matches 341; Conservative 0; Mismatches 22; Indels 6; Gaps 1;

QY 1 CAGGTTACTCTGAAAGAGTCTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCAGTCTG 60
 Db |||||
 QY 58 CAGGTTACTCTGAAAGAGTCTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCAGTCTG 117
 Db |||||
 QY 61 ACTTGTCTTTCTCTGGGTTTTCACCTGAGCACCTTCTGGTATGGGTGTGAGTGTGATTCGA 120
 Db |||||
 QY 118 ACTTGTCTTTCTCTGGGTTTTCACCTGAGCACCTTCTGGTATGGGTGTGAGTGTGATTCGT 177
 Db |||||
 QY 121 CAGCCTTTCAAGAAAGGCTCTGGAGTGGCTGGCACACATTTACTGGGATGATGACAAGGC 180
 Db |||||

Db 178 CAGCCTTCAGGAAGGGCTCTGGAGTGGCTGGCACACATTTACTGGGATGATGACAAGCGC 237
Qy 181 TATAACCCATCCCTGAAGAGCGGGCTTCAATCTCCAGGATACCTCCAGCAACAGGTA 240
Db 238 TATAACCCATCCCTGAAGAGCGGGCTCAAACTCCAGGATACCTCCAGAAAGCAGGTA 297
Qy 241 TTCTCTCAAGATCACCAAGTGTGGACACTCGAGATACCTGCCACATATCTACTGTCTCGAAGG 300
Db 298 TTCTCTCAAGATCACCAAGTGTGGACCTCGAGATACCTGCCACATATCTACTGTCTCGAAGG 357
Qy 301 GTC-----TCTCTAAGTCTTGTATGAGTACTGGGGTCAAGGAACCTCAAGTCAAC 354
Db 358 CCATTACTCCGGTACTAGTCGATGCTATGGACTACTGGGGTCAAGGAACCTCAAGTCAAC 417
Qy 355 GTCTCTCTCA 363
Db 418 GTCTCTCTCA 426

RESULT 6

US-09-995-529-11
; Sequence 11, Application US/09995529
; Publication No. US20030099655A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(369)
US-09-995-529-11

Query Match 82.4%; Score 299; DB 11; Length 369;

Best Local Similarity 50.2%; Pred. No. 1.7e-92;
Matches 333; Conservative 0; Mismatches 30; Indels 6; Gaps 1;

Qy 1 CAGGTTACTCTGAAAGAGTCTGGCCCTGGGATATTGCAGCCCTCCAGACCCCTCAGTCTG 60
Db 1 CAGGTTACTCTGAAAGAGTCTGGCCCTGGGATATTGCAGCCCTCCAGACCCCTCAGTCTG 60
Qy 61 ACTTGTTCTTTCTCTGGGTTTTCACGTAGCAGCACTCTGGTATGGGTGAGCTGGATTGGA 120
Db 61 ACTTGTTCTTTCTCTGGGTTTTCACGTAGCAGCACTCTGGTATGGGTGAGCTGGATTGCG 120
Qy 121 CAGCCTTCAGAAAGGGTCTGGAGTGGCTGGCACACATTTACTGGGATGATGACAAGCGC 180
Db 121 CAGCCTTCAGAGAGGGTCTAGAGTGGCTGGCAGACATTTGGTGGATGACATAAGTAC 180
Qy 181 TATAACCCATCCCTGAAGAGCGGGCTTACAATCTCCAGGATACCTCCAGCAACCAAGGTA 240
Db 181 TATAACCCATCCCTGAAGAGCGGGCTCACAATCTCCAGGATACCTCCAGCAACCAAGGTA 240
Qy 241 TTCTCTAAGATCACCAAGTGTGGACACTCGAGATACCTGCCACATCTACTGTCTCGAAGG 300
Db 241 TTCTCTAAGATCACCAAGTGTGGACACTCGAGATACCTGCCACATCTACTGTCTCGAAGG 300
Qy 301 G-----TCTCTCTAAGTCTTGTATGAGTACTGGGGTCAAGGAACCTCAGTCAAC 354
Db 301 GCTAACTATGTAACCCCTACTATGCTATGAGTACTGTGGGTCAAGGAACCTCAGTCAAC 360
Qy 355 GTCTCTCTCA 363

Db 361 GTCTCTCTCA 369

RESULT 7

US-09-881-823-7
; Sequence 7, Application US/09881823
; Patent No. US20020068066A1
; GENERAL INFORMATION:
; APPLICANT: SHI, WENYUAN
; APPLICANT: ANDERSON, MAXWELL
; APPLICANT: MORRISON, SHERIE
; APPLICANT: TRINH, RYAN
; APPLICANT: WIMS, LETITIA
; APPLICANT: CHEN, LI
; TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries
; FILE REFERENCE: 22851-032
; CURRENT APPLICATION NUMBER: US/09/881,823
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 07/378,577
; PRIOR FILING DATE: 1999-08-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 465
; TYPE: DNA
; ORGANISM: Murine
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)...(441)
US-09-881-823-7

Query Match 78.3%; Score 284.4; DB 9; Length 465;

Best Local Similarity 88.0%; Pred. No. 1.9e-87;
Matches 322; Conservative 0; Mismatches 41; Indels 3; Gaps 1;

Qy 1 CAGGTTACTCTGAAAGAGTCTGGCCCTGGGATATTGCAGCCCTCCAGACCCCTCAGTCTG 60
Db 70 CAGGTTACTCTGAAAGAGTCTGGCCCTGGGATATTGCAGCCCTCCAGACCCCTCAGTCTG 129
Qy 61 ACTTGTTCTTTCTCTGGGTTTTCACGTAGCAGCACTCTGGTATGGGTGAGCTGGATTGGA 120
Db 130 ACTTGTTCTTTCTCTGGGTTTTCACGTAGCAGCACTCTGGTATGGGTGAGCTGGATTGCG 189
Qy 121 CAGCCTTCAGAAAGGGTCTGGAGTGGCTGGCACACATTTACTGGGATGATGACAAGCGC 180
Db 190 CAGCCTTCAGAGAGGGTCTGGAGTGGCTGGCACACATTTGGTGGATGATATATAGTAC 249
Qy 181 TATAACCCATCCCTGAAGAGCGGGCTTACAATCTCCAGGATACCTCCAGCAACCAAGGTA 240
Db 250 TATAACACAGTCTCTGAAGAGCGGGCTCACAATCTCCAGGATACCTCCAGCAACCAAGGTA 309
Qy 241 TTCTCTAAGATCACCAAGTGTGGACACTCGAGATACCTGCCACATCTACTGTCTCGAAGG 300
Db 310 TTCTCTAAGATCGCCAGTGTGGACACTCGAGATACCTGCCACATCTACTGTCTCGCGAATA 369
Qy 301 GTCTCTCTAACTGGCT---ATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCAACGTC 357
Db 370 GAGGGGGCTCGGGCTACGATGTTATGGACTACTGGGGTCAAGGAATCTCAGTCAACGTC 429
Qy 358 TCCTCA 363
Db 430 TCCTCA 435

RESULT 8

US-10-323-903-4
; Sequence 4, Application US/10323903
; Publication No. US2003022832A1
; GENERAL INFORMATION:
; APPLICANT: FISCHER, GERALD WALTER
; APPLICANT: SCHUMAN, RICHARD F.
; APPLICANT: MOND, JAMES JACOB

APPLICANT: KOKAI-KUN, JOHN FITZGERALD
APPLICANT: POSTER, SIMON
APPLICANT: STINSON, JEFFREY R.
TITLE OF INVENTION: MULTIFUNCTIONAL MONOCLONAL ANTIBODIES DIRECTED TO
FILE REFERENCE: 07787.0059
CURRENT APPLICATION NUMBER: US/10/323,903
CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: 60/343,444
PRIOR FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/097,055
PRIOR FILING DATE: 1998-06-15
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 357
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(357)
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA encoding
US-10-323-903-4

Query Match 74.6%; Score 270.8; DB 12; Length 357;
Best Local Similarity 94.3%; Pred. No. 8.5e-83;
Matches 281; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCCCTCAGTCTG 60
Db 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCCCTCAGTCTG 60
QY 61 ACTTGTCTTCTCTGGGTTTTCACGTAGCAGCACTTCTGGTATGGGTGAGCTGGATTGGA 120
Db 61 ACTTGTCTTCTCTGGGTTTTCACGTAGCAGCACTTCTGGTATGGGTGAGCTGGATTGCT 120
QY 121 CAGCCTTCAGAAAGGCTCTGGAGTGGCTGGGACACATTTACTGGGATGATGACAGCGC 180
Db 121 CAGCCTTCAGAAAGGCTCTGGAGTGGCTGGGACACATTTACTGGGATGATGACAGCGC 180
QY 181 TATAACCCATCCCTGAAGAGCCGGCTTACAATCTCAAGGATACCTCCAGCAACCCAGGTA 240
Db 181 TATAACCCATCCCTGAAGAGCCGACTCAGAGTCTCAAGGATACCTCCAGCAACCCAGGTC 240
QY 241 TTCTCAAGATCACCAGTGTGGACACTCGAGATCTGCGACATCTACTGTGCTCGAA 298
Db 241 TTCTCAAGATCACCAGTGTGGGCACTGCGAGATCTGCGACATCTACTGTGCTCGAA 298

RESULT 9
US-09-764-304-1
Sequence 1, Application US/09764304
Patent No. US2002026036A1
GENERAL INFORMATION:
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUWANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/09/764,304
CURRENT FILING DATE: 2001-01-19
EARLIER APPLICATION NUMBER: 09/225,322
EARLIER FILING DATE: 1999-01-05
EARLIER APPLICATION NUMBER: US 08/454,680
EARLIER FILING DATE: 1995-05-31
EARLIER APPLICATION NUMBER: US 08/408,133
EARLIER FILING DATE: 1995-03-21
EARLIER APPLICATION NUMBER: US 08/292,178
EARLIER FILING DATE: 1994-08-17

EARLIER APPLICATION NUMBER: US07/947,674
EARLIER FILING DATE: 1992-09-17
EARLIER APPLICATION NUMBER: JP 3-238375
EARLIER FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 812
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Rat Hybridoma
FEATURE:
NAME/KEY: TATA signal
LOCATION: (256)..(262)
NAME/KEY: sig_peptide
LOCATION: (300)..(440)
NAME/KEY: CDS
LOCATION: (300)..(344)
NAME/KEY: CDS
LOCATION: (429)..(806)
NAME/KEY: mat_peptide
LOCATION: (300)..(806)
NAME/KEY: intron
LOCATION: (345)..(428)
US-09-764-304-1
Query Match 69.1%; Score 250.8; DB 9; Length 812;
Best Local Similarity 82.2%; Pred. No. 8.8e-76;
Matches 301; Conservative 0; Mismatches 62; Indels 3; Gaps 1;
QY 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCCCTCAGTCTG 60
Db 441 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCCCTCAGTCTG 500
QY 61 ACTTGTCTTCTCTGGGTTTTCACGTAGCAGCACTTCTGGTATGGGTGAGCTGGATTGGA 120
Db 501 ACTTGTCTTCTCTGGGTTTTCACGTAGCAGCACTTGGTATGGGTGAGCTGGATTGCT 560
QY 121 CAGCCTTCAGAAAGGCTCTGGAGTGGCTGGGACACATTTACTGGGATGATGACAGCGC 180
Db 561 CAGGTTCTCAGGAGAGGCTCTGGAGTGGCTGGGACAACTTTGGTGGAGTGTGCTAAAGTAC 620
QY 181 TATAACCCATCCCTGAAGAGCCGGCTTACAATCTCAAGGATACCTCCAGCAACCCAGGTA 240
Db 621 TACATCCATCTCTGAAGAACCCGCTCACAATCTCAAGGACACCTCCACACACCAAGCA 680
QY 241 TTCTCAAGATCACCAGTGTGGACACTCGAGATCTGCGACATCTACTGTGCTCGAAGG 300
Db 681 TTCTCAAGATCACCATATATGACACTGCGAGATCTGCCATATATCTACTGTGCTGGAGA 740
QY 301 GTCTCTCTAACTGCTATGCTA--TGGACTACTGGGGTCAAGGAACCTCAGTCACCGTC 357
Db 741 GGGCTAGGAGGTATAGTGGCTTTGATTTCTGGGGCCACCGAGTCTAGTGCACAGTC 800
QY 358 TCCTCA 363
Db 801 TCCTCA 806
RESULT 10
US-10-166-626-1
Sequence 1, Application US/10166626
Publication No. US20030166876A1
GENERAL INFORMATION:
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUWANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/10/166,626

CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: US/09/225,322B
PRIOR FILING DATE: 1999-01-05
PRIOR APPLICATION NUMBER: US 08/454,680
PRIOR FILING DATE: 1995-05-31
PRIOR APPLICATION NUMBER: US 08/408,133
PRIOR FILING DATE: 1995-03-21
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR FILING DATE: 1994-08-17
PRIOR APPLICATION NUMBER: US07/947,674
PRIOR FILING DATE: 1992-09-17
PRIOR APPLICATION NUMBER: JP 3-238375
PRIOR FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 1
LENGTH: 812
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Rat Hybridoma
NAME/KEY: TATA signal
LOCATION: (256)..(262)
FEATURE:
NAME/KEY: sig peptide
LOCATION: (300)..(440)
FEATURE:
NAME/KEY: CDS
LOCATION: (300)..(344)
FEATURE:
NAME/KEY: CDS
LOCATION: (429)..(806)
FEATURE:
NAME/KEY: mat_peptide
LOCATION: (300)..(806)
FEATURE:
NAME/KEY: intron
LOCATION: (346)..(428)
US-10-166-626-1

Query Match 69.1%; Score 250.8; DB 13; Length 812;
Best Local Similarity 82.2%; Pred. No. 8.8e-76;
Matches 301; Conservative 0; Mismatches 62; Indels 3; Gaps 1;
QY 1 CAGGTTACTCTGAAGAGTCTGSCCTGGGATATTGACGCTCCAGACCCCTCAGTCTG 60
DB 441 CAGGTTACTCTGAAGAAATCTGCCCTGGGATATTGACGCTCCAGACCCCTCAGTCTG 500
QY 61 ACTTGTCTTTCTCTGGTTTCTCAGTCTGAGTCTGATGGTGTGAGTGGATTGGA 120
DB 501 ACTTGTCTTTCTCTGGTTTCTCAGTCTGAGTCTGATGGTGTGAGTGGATTGCG 560
QY 121 CAGCCTTCAGGAAGGCTCTGGAGTGGCTGGCACATTTACTGGATGATGACAGCGC 180
DB 561 CAGTCTTCAGGAAGGCTCTGGAGTGGCTGGCACATTTACTGGATGATGACAGCGC 620
QY 181 TATAACCCATCCCTGGAAGACCGGCTTACAACTTCCAAGGATACCTCCAGCAACAGGTA 240
DB 621 TACAATCCATCTCTGAAGAAACCGGCTCACAATCTCCAAGGACACCTCCACACCAAGCA 680
QY 241 TTCTCTCAGATCACCAGTCTGGACATCTCGAGATACCTGCCACATCTACTGTGCTGAAG 300
DB 681 TTCTCTCAGATCACCAGTCTGGACATCTCGAGATACCTGCCACATCTACTGTGCTGAAG 740
QY 301 GTCTCTTAAGTCCCTATGCTA---TGGACTACTGGGGTCAAGGAACCTCAGTCAACGTC 357
DB 741 GGGGCTACGGAGGTATAGTGAAGCTTTGATTTACTGGGGCCACGGAGTCATGCTCAGTTC 800
QY 358 TCCTCA 363
DB 801 TCCTCA 806

RESULT 11
US-10-195-752-16
Sequence 16, Application US/10195752
Publication No. US20030077276A1
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
KOIKE, MASAMICHI
SHITARA, KENYA
HANAI, NOBUO
KUWANA, YOSHIHISA
HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHUYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/195,752
FILING DATE: 16-Jul-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/393,385B
FILING DATE: 27-JUN-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 812 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: HYBRIDOMA KM50
FEATURE:
NAME/KEY: TATA signal
LOCATION: 261..267
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-195-752-16
Query Match 69.1%; Score 250.8; DB 15; Length 812;
Best Local Similarity 82.2%; Pred. No. 8.8e-76;
Matches 301; Conservative 0; Mismatches 62; Indels 3; Gaps 1;
QY 1 CAGGTTACTCTGAAGAGTCTGSCCTGGGATATTGACGCTCCAGACCCCTCAGTCTG 60
DB 441 CAGGTTACTCTGAAGAAATCTGCCCTGGGATATTGACGCTCCAGACCCCTCAGTCTG 500
QY 61 ACTTGTCTTTCTCTGGTTTCTCAGTCTGAGTCTGATGGTGTGAGTGGATTGGA 120
DB 501 ACTTGTCTTTCTCTGGTTTCTCAGTCTGAGTCTGATGGTGTGAGTGGATTGCG 560
QY 121 CAGCCTTCAGGAAGGCTCTGGAGTGGCTGGCACATTTACTGGGATGATGACAGCGC 180
DB 561 CAGTCTTCAGGAAGGCTCTGGAGTGGCTGGCACATTTACTGGGATGATGACAGCGC 620
QY 181 TATAACCCATCCCTGGAAGACCGGCTTACAACTTCCAAGGATACCTCCAGCAACAGGTA 240
DB 621 TACAATCCATCTCTGAAGAAACCGGCTCACAATCTCCAAGGACACCTCCACACCAAGCA 680
QY 241 TTCTCTCAGATCACCAGTCTGGACATCTCGAGATACCTGCCACATCTACTGTGCTGAAG 300

Db 681 TTCTCAAGATCAACCAATATGGACACTGCAGATACTGCCATATACTACTGTGTGGAGA 740
Qy 301 GTCTCTTAAGTCTGCTATGCTA---TGGACTACTGGGGTCAAGGAACCTCAGTCACGGTC 357
Db 741 GGGCTAGGAGGTATATGAGCTTTTGAATTACTTGGGGCCACGAGTCTATGGTCACAGTC 800
Qy 358 TCCTCA 363
Db 801 TCCTCA 806

RESULT 12

US-10-265-713-1
; Sequence 1, Application US/10265713
; Publication No. US20030095964A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KIWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/265,713
; PRIOR FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 812
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Rat Hybridoma
; NAME/KEY: TATA signal
; LOCATION: (256)..(262)
; NAME/KEY: sig_peptide
; LOCATION: (300)..(440)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (300)..(344)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (429)..(806)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (300)..(806)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (346)..(428)
US-10-265-713-1

Query Match 69.1%; Score 250.8; DB 15; Length 812;
Best Local Similarity 82.2%; Pred. No. 8.9e-76;
Matches 301; Conservative 0; Mismatches 62; Indels 3; Gaps 1;

Qy 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCAGTCTG 60
Db 441 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCAGTCTG 500

Qy 61 ACTTGCTCTTCTCTGCGGTTTTCACTGAGCACTTCTGATGGGTGCTGAGCTGGATCGA 120
Db 501 ACTTGCTCTTCTCTGCGGTTTTCACTGAGCACTTATGATGTGTGGGTGGATTGCT 560
Qy 121 CAGCCTTCAGGAAGGGTCTGGAGTGGCTGGCACACATTTTACTGGGATGATGACAAGCGC 180
Db 561 CAGTCTTCAGGAAGGGTCTGGAGTGGCTGGCAACGTTTGGTGGAGTGTGCTAAGTAC 620
Qy 181 TATRACCCATCCCTGAAGAGCGGCTTACATCTCCAGGATACCTCCAGAACCGGTA 240
Db 621 TACATCCATCTCTGAAAACCGGCTCAATCTCCAAAGACACCTCCCAACCAAGCA 680
Qy 241 TTCCTCAAGATCACCAGTGTGGACACTCGAGATACTGCCACATCTACTGTGCTCGAAG 300
Db 681 TTCCTCAAGATCACCAGTGTGGACACTCGAGATACTGCCATATCTACTGTGCTGGAGA 740
Qy 301 GTCTCTTAAGTCTGCTATGCTA---TGGACTACTGGGGTCAAGGAACCTCAGTCACGGTC 357
Db 741 GGGCTACGGAGGTATAGTGAAGTTGATTACTTGGGGCCACGAGTCTATGGTCACAGTC 800
Qy 358 TCCTCA 363
Db 801 TCCTCA 806

RESULT 13

US-10-255-478-50
; Sequence 50, Application US/10255478
; Publication No. US20030165498A1
; GENERAL INFORMATION:
; APPLICANT: Mezes, Peter S.
; APPLICANT: Richard, Ruth A.
; APPLICANT: Johnson, Kimberly S.
; APPLICANT: Schlom, Jeffrey
; APPLICANT: Kashmiri, Syed V.S.
; APPLICANT: Shu, Liming
; APPLICANT: Padlan, Eduardo A.
; TITLE OF INVENTION: Composite Antibodies of Humanized Human Subgroup IV Light Chain
; FILE REFERENCE: 37777E
; CURRENT APPLICATION NUMBER: US/10/255,478
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US/08/961,309
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/030,173
; PRIOR FILING DATE: 1996-10-31
; PRIOR APPLICATION NUMBER: US 08/261,354
; PRIOR FILING DATE: 1994-06-16
; PRIOR APPLICATION NUMBER: US 07/964,536
; PRIOR FILING DATE: 1992-10-20
; PRIOR APPLICATION NUMBER: US 07/510,697
; PRIOR FILING DATE: 1990-07-17
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 50
; LENGTH: 423
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: B17X2 VH coding sequence
; LOCATION: 7..423
; OTHER INFORMATION: DNA encoding the heavy chain variable region of the anti-N-
; OTHER INFORMATION: acetylglucosamine antibody, B17X2
US-10-255-478-50

Query Match 52.7%; Score 191.4; DB 13; Length 423;
Best Local Similarity 72.2%; Pred. No. 2e-55;
Matches 262; Conservative 0; Mismatches 92; Indels 9; Gaps 1;

Qy 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCAGTCTG 60
Db 64 CAGATCACCTTGAGAGTCTGTCTTACNCTGGTGAACCCACACAGACCTTCAGGCTG 123

QY 61 ACTTGTTCTTCTCTGGGTTTCACTGAGCACTCTGGTATGGGTGTCAGCTGGATTGCA 120
|||
Db 124 ACTGACCTTCTCTGGGTTTCACTGAGCACTCATGGAGTGGGTGTGGCTGGATCCGT 183
|||
QY 121 CAGCCTTCAGGAAAGGTTCTGGAGTGGCTGGGCACACATTTACTGGGATGATGACAGCGC 180
|||
Db 184 NNNNNCCAGGAAAGCCCTGGAGTGGCTTGCACTCAITTTATTGGGATGATGATAAGCGC 243
|||
QY 181 TATAACCCATCCCTGAAGAGCGGCTTCAATCTCCAAGGATACCTCCAGCAACCCAGGTA 240
|||
Db 244 TACAGCCCATCTCTGAAGAGAGGCTCACATCAACCAAGGACACTCCAAAACAGGTG 303
|||
QY 241 TTCTCAAGATCACCAAGTGTGGACACTCGAGATAGTCCACATATCTATGTCGTGGAAG 300
|||
Db 304 ATCCTTACAATGACCAACATGAGCCCTGTGGACACAGCCACATATTTATGTCACACGGG 363
|||
QY 301 GTCTCTTAACCTGCTATGCTATGGACTACTGGGTCTAGGAGCACTCAGTCACCTCTCC 360
|||
Db 364 CT-----GCCATCTATGGTTAAGAACTGGGGCCAGGACACCGGTACCGTCTCC 414
|||
QY 361 TCA 363
|||
Db 415 TCA 417

RESULT 14

US-10-072-301-22
; Sequence 22, Application US/10072301
; Publication No. US20030152913A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEF
; FILE REFERENCES: 25636-718
; CURRENT APPLICATION NUMBER: US/10/072,301
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 22
; LENGTH: 759
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.150.24
US-10-072-301-22

Query Match 50.4%; Score 183; DB 13; Length 759;
Best Local Similarity 76.3%; Pred. No. 1.9e-52;
Matches 225; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
QY 1 CAGGTACTCTGAAAGAGTCTGCCCTGGGATATTCAGCCCTCCAGACCCCTCAGTCTG 60
|||
Db 1 CAGGTACCTTGAAGGAGTCTGGTCTTACGCTGGTGAACCCACACAGACCCCTCAGCTG 60
|||
QY 61 ACTTGTTCTTCTCTGGGTTTCACTGAGCACTCTGGTATGGGTGTCAGCTGGATTGCA 120
|||
Db 61 ACTGCACTTCTCTGGGTTTCACTCAGAACTACTGGAGAGGTTGTGGCTGGTCCGT 120
|||
QY 121 CAGCCTTCAGGAAAGGTTCTGGAGTGGCTGGGCACATTTACTGGGATGATGACAGCGC 180
|||
Db 121 CAGCCCCCAGGAAAGCCCTGGAATGGCTTGCACTCAITTTATTGGGATGATGATAAGCGC 180
|||
QY 181 TATAACCCATCCCTGAGAGCGGCTTACAATCTCCAAGGATACCTCCAGCAACCCAGGTA 240
|||
Db 181 TACAGCCCATCTCTGAAGAGAGGCTCACCATCACCAGGACACCTCCAAAAGAGGTTG 240
|||
QY 241 TTCTCAAGATCACCAAGTGTGGACACTCGAGATACCTGCCACATACCTACTGTGCTC 295
|||
Db 241 GTCTTACAATGACCAACGTGGACCCAGCGGACACAGCCACCTATTACTGTACAC 295
|||

RESULT 15
US-10-072-301-30
; Sequence 30, Application US/10072301
; Publication No. US20030152913A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEF
; FILE REFERENCES: 25636-718
; CURRENT APPLICATION NUMBER: US/10/072,301
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 30
; LENGTH: 759
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.150.24 Variant
US-10-072-301-30

Query Match 50.4%; Score 183; DB 13; Length 759;
Best Local Similarity 76.3%; Pred. No. 1.9e-52;
Matches 225; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
QY 1 CAGGTACTCTGAAAGAGTCTGCCCTGGGATATTCAGCCCTCCAGACCCCTCAGTCTG 60
|||
Db 1 CAGGTACCTTGAAGGAGTCTGGTCTTACGCTGGTGAACCCACACAGACCCCTCAGCTG 60
|||
QY 61 ACTTGTTCTTCTCTGGGTTTCACTGAGCACTCTGGTATGGGTGTCAGCTGGATTGCA 120
|||
Db 61 ACTGCACTTCTCTGGGTTTCACTCAGAACTACTGGAGAGGTTGTGGCTGGTCCGT 120
|||
QY 121 CAGCCTTCAGGAAAGGTTCTGGAGTGGCTGGGCACATTTACTGGGATGATGACAGCGC 180
|||
Db 121 CAGCCCCCAGGAAAGCCCTGGAATGGCTTGCACTCAITTTATTGGGATGATGATAAGCGC 180
|||
QY 181 TATAACCCATCCCTGAGAGCGGCTTACAATCTCCAAGGATACCTCCAGCAACCCAGGTA 240
|||
Db 181 TACAGCCCATCTCTGAAGAGAGGCTCACCATCACCAGGACACCTCCAAAAGAGGTTG 240
|||
QY 241 TTCTCAAGATCACCAAGTGTGGACACTCGAGATACCTGCCACATACCTACTGTGCTC 295
|||
Db 241 GTCTTACAATGACCAACGTGGACCCAGCGGACACAGCCACCTATTACTGTACAC 295
|||

Search completed: January 14, 2004, 19:01:59
Job time : 218.81 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 14, 2004, 17:47:02 ; Search time 37.1905 Seconds
(without alignments)
516.420 Million cell updates/sec

Title: US-09-759-112a-7

Perfect score: 633

Sequence: 1 QVTLKESGPIQLPSQTLSL.....SLTAYAMDYWGQTSVTWS 121

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
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24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	633	100.0	121	AA018528	Murine Mab 1F7 hea
2	569	89.9	140	AA070190	Mouse Mab 3B9 heav
3	569	89.9	140	AA023768	Heavy chain variab
4	569	89.9	140	AA018121	Heavy chain sequen
5	569	89.9	141	AA070191	Chimeric antibody
6	569	89.9	141	AA023769	Heavy chain variab
7	569	89.9	141	AA018125	Chimeric 3B9 monoc
8	567.5	89.7	246	AA058612	IL-6 binding inhib
9	551	87.0	142	ABG76934	Mouse 10D5 VH prot

10	546.5	86.3	122	15	AA054101	Humanised Mab H-ch
11	522.5	82.5	120	17	AA088109	Murine anti-Protei
12	522.5	82.5	139	17	AA088107	Murine anti-Protei
13	521.5	82.4	139	16	AA067685	Mouse heavy chain
14	520	82.1	121	23	ABG67188	Human IgG1 antibod
15	516	81.5	121	20	AA025396	WO9932630 Seq ID 3
16	516	81.5	259	21	AA090778	Antiviral scFv-ant
17	516	81.5	259	22	AA070895	TMV 54K protein de
18	514	81.2	123	21	AA021367	Mouse antibody 13G
19	509	80.4	470	21	AAU77289	Protein #2 in inve
20	506.5	80.0	120	17	AA020899	Anti-RSV F glycopr
21	506.5	80.0	120	23	ABG31433	Amino acid sequenc
22	506.5	80.0	143	23	AB079728	Anti-Streptococcus
23	505.5	79.9	143	15	AA054092	Sequence of mouse
24	502	79.3	141	16	AA070192	Humanized antibody
25	502	79.3	141	20	AA023770	Heavy chain variab
26	502	79.3	141	20	AA018117	Heavy chain sequen
27	500	79.0	121	20	AA023780	Heavy chain variab
28	500	79.0	121	20	AA018122	Heavy chain sequen
29	494	78.0	123	24	ABP58285	Humanised 10D5 ant
30	494	78.0	453	24	ABP58287	Humanised 10D5 ant
31	494	78.0	472	24	ABP58289	Humanised 10D5 ant
32	476	75.2	123	24	ABP58283	Humanised 10D5 ant
33	470.5	74.3	141	14	AA033255	Rat immunoglobulin
34	470.5	74.3	141	15	AA033339	RM50 cell-derived
35	470.5	74.3	141	20	AA028367	RM50 Rat immunogl
36	470.5	74.3	141	21	AA016266	Rat activated immu
37	468.5	74.0	120	22	AA010476	Humanised antibody
38	468.5	74.0	120	22	AA063243	Mouse anti-RSV ant
39	468.5	74.0	450	23	ABP56562	Human RSV antibody
40	468.5	74.0	450	24	ABU94455	Respiratory syncyt
41	467.5	73.9	120	23	ABG31432	Humanised CDR-graf
42	466.5	73.7	120	17	AA032088	CDR-grafted anti-R
43	466.5	73.7	120	22	AA063259	Anti-RSV antibody
44	466.5	73.7	120	22	AA063261	Anti-RSV antibody
45	466.5	73.7	120	22	AA063265	Anti-RSV antibody

ALIGNMENTS

RESULT 1

AA018528

ID AA018528 standard; Protein; 121 AA.

AC AA018528;

DT 11-OCT-2002 (first entry)

DE Murine Mab 1F7 heavy chain.

KW Mouse; 1F7; antibody; immune modulator; anti-HIV antibody; CDR;
complementarity determining region; framework-determining region;
FR; heavy chain; light chain; HIV infection.

OS Mus sp.

PN WO200255668-A2.

PD 18-JUL-2002.

PF 11-JAN-2002; 2002WO-US00927.

PR 11-JAN-2001; 2001US-0759112.

PA (IMMP-) IMMUPHERON INC.

PI Muller S, Kohler H;

DR WPI; 2002-590668/63.

XX N-PSDB; AAL48652.

PT New polynucleotide encoding a complementarity- or framework-determining

PT region of an anti-idiotypic antibody that binds to human or primate
 PT anti-human immunodeficiency virus (HIV) antibodies, for use in
 PT vaccines against HIV

XX Disclosure; Page 18-19; 27pp; English.

XX The present invention relates to coding sequences of the murine IF7
 CC anti-idiotypic antibody complementarity-determining region (CDR) or
 CC framework-determining region (FR). The antibody binds to human or primate
 CC anti-human immunodeficiency virus (HIV) antibodies and can be used in the
 CC treatment of HIV infection. The present sequence is the IF7 heavy chain.

XX Sequence 121 AA;

Query Match 100.0%; Score 633; DB 23; Length 121;
 Best Local Similarity 100.0%; Pred. No. 7,3e-55;
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVTLKESGPGIQLPSQTLTSLTCSFGSFLSTSGMGVSWIRQPSGKLEWLAHIYWDGDKR 60
 DB 1 QVTLKESGPGIQLPSQTLTSLTCSFGSFLSTSGMGVSWIRQPSGKLEWLAHIYWDGDKR 60
 QY 61 YNPGLKSLRTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQGSVTVS 120
 DB 61 YNPGLKSLRTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQGSVTVS 120

QY 121 S 121

DB 121 S 121

RESULT 2

ID AAR70190 standard; Protein; 140 AA.

XX AAR70190;

XX 25-MAR-2003 (updated)

DT 20-SEP-1995 (first entry)

DE Mouse MAb 3B9 heavy chain.

XX Chimeric antibody; humanized antibody; antibody engineering;
 XX monoclonal antibody; MAb; interleukin-4; IL-4; allergy.

OS Mus sp.

XX Key Location/Qualifiers

FT Peptide 1..19

FT /label= Sig_peptide

FT Region 50..56

FT /label= CDR

FT /note= "complementarity determining region"

FT Region 71..86

FT /label= CDR

FT /note= "complementarity determining region"

FT Region 119..129

FT /label= CDR

FT /note= "complementarity determining region"

XX WO9507301-A1.

PN 16-MAR-1995.

XX 07-SEP-1994; 94WO-US10308.

XX 07-SEP-1993; 93US-0117366.

XX 14-OCT-1993; 93US-0136783.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Gross MS, Holmes SD, Sylvester DR;

PI WPI; 1999-429500/36.

XX WPI; 1995-123387/16.
 DR N-PSDB; AAQ83491.

XX Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
 PT from high affinity mAbs - useful in treatment of IL-4-mediated
 PT and IgE-mediated allergic conditions

XX Disclosure; Fig.2; 97pp; English.

XX Spleen cells from mice immunized with human IL-4 were used to prepare
 CC hybridomas, which were screened for anti-IL-4 Mab secretion. Only
 CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy
 CC chains were cloned into pGEM7f+ and transformed into E. coli
 CC DH5-alpha. The clones were sequenced (AAQ83490-91), and used for
 CC antibody engineering.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 140 AA;

Query Match 89.9%; Score 569; DB 16; Length 140;

Best Local Similarity 90.1%; Pred. No. 1.8e-48;

Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVTLKESGPGIQLPSQTLTSLTCSFGSFLSTSGMGVSWIRQPSGKLEWLAHIYWDGDKR 60
 DB 20 QVTLKESGPGIQLPSQTLTSLTCSFGSFLSTSGMGVSWIRQPSGKLEWLAHIYWDGDKR 79

QY 61 YNPGLKSLRTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQGSVTVS 120

DB 80 YNPGLKSLRTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQGSVTVS 139

QY 121 S 121

DB 140 S 140

RESULT 3

AAAY23768

ID AAAY23768 standard; Protein; 140 AA.

XX AAAY23768;

XX 13-SEP-1999 (first entry)

XX Heavy chain variable region of murine IL-4 antibody 3B9.

XX Heavy chain variable region; interleukin-4; IL-4; antibody 3B9;
 KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;
 KW immunoglobulin E-mediated allergic reaction; allergic rhinitis;
 KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
 KW rheumatoid arthritis; host-versus-graft disease; renal disease;
 KW allergy.

XX Mus sp.

PN US5928904-A.

XX 27-JUL-1999.

XX 07-JUN-1995; 95US-0483632.

XX 07-JUN-1995; 95US-0483632.

XX 07-SEP-1993; 93US-0117366.

XX 14-OCT-1993; 93US-0136783.

XX 07-SEP-1994; 94WO-US10308.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Gross MS, Holmes SD, Sylvester DR;

XX WPI; 1999-429500/36.

DR N-PSDB; AAX85885.

XX New DNA molecules encoding recombinant antibodies useful for
PT treating IL4-mediated conditions

PS Example 3; Fig 2; 50pp; English.

XX The present sequence represents the heavy chain variable region of
CC murine interleukin-4 (IL-4) antibody 3B9. The sequences are used
CC in the production of chimeric and humanised IL-4 monoclonal antibodies.
CC The antibodies of the invention are used in therapeutic and
CC pharmaceutical compositions for treating IL-4 mediated and
CC immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis,
CC conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock,
CC rheumatoid arthritis, host-versus-graft disease and renal disease.
CC They are also useful in the diagnosis of an allergy or condition
CC associated with excess IL-4 production through the measurement e.g. by
CC ELISA of circulating endogenous IL-4 levels in humans.

XX Sequence 140 AA;

Query Match 89.9%; Score 569; DB 20; Length 140;
Best Local Similarity 90.1%; Pred. No. 1.8e-48;

Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVTLKESGPGILQPSQTLSTLCSPGFSLSSTSGMVGVSWIRQPSGKGLEWLAHIYWDGDKR 60

DB 20 QVTLKESGPGILQPSQTLSTLCSPGFSLSSTSGMVGVSWIRQPSGKGLEWLAHIYWDGDKR 79

QY 61 YNPSLKSLRTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQTSVTVS 120

DB 80 YNPSLKSLRTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQTSVTVS 139

QY 121 S 121

DB 140 S 140

RESULT 4

AAY18121

ID AAY18121 standard; Protein; 140 AA.

XX AC AAY18121;

XX 11-AUG-1999 (first entry)

XX Heavy chain sequence for murine 3B9 antibody.

XX Antibody; interleukin-4; IL4; immunoglobulin E; IGE mediated disease;
KW allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;
KW atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;
KW autoimmune disease; graft versus host disease.

XX OS Mus sp.

XX US5914110-A.

XX 22-JUN-1999.

XX 07-JUN-1995; 95US-0483636.

XX 07-JUN-1995; 95US-0483636.

XX 07-SEP-1993; 93US-0117366.

XX 14-OCT-1993; 93US-0136783.

XX 07-SEP-1994; 94WO-US10308.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Gross MS, Holmes SD, Sylvester DR;

XX WPI; 1999-370482/31.

XX N-PSDB; AAX79520.

XX Recombinant IL4 antibodies

XX Claim 24; Fig 2; 50pp; English.

XX This sequence represents the heavy chain of the murine 3B9
CC antibody of the invention. The antibody is a chimeric or
CC humanised interleukin-4 (IL4) monoclonal antibody for the treatment of
CC immunoglobulin E (IGE) mediated diseases. The antibodies are useful for
CC the treatment of allergic disorders such as allergic rhinitis,
CC conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock.
CC The antibodies are also useful for regulating B and T cell proliferation
CC and as such are useful in the treatment of autoimmune diseases and graft
CC versus host disease.

XX Sequence 140 AA;

Query Match 89.9%; Score 569; DB 20; Length 140;
Best Local Similarity 90.1%; Pred. No. 1.8e-48;

Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVTLKESGPGILQPSQTLSTLCSPGFSLSSTSGMVGVSWIRQPSGKGLEWLAHIYWDGDKR 60

DB 20 QVTLKESGPGILQPSQTLSTLCSPGFSLSSTSGMVGVSWIRQPSGKGLEWLAHIYWDGDKR 79

QY 61 YNPSLKSLRTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQTSVTVS 120

DB 80 YNPSLKSLRTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQTSVTVS 139

QY 121 S 121

DB 140 S 140

RESULT 5

AAR70191

ID AAR70191 standard; Protein; 141 AA.

XX AC AAR70191;

XX 25-MAR-2003 (updated)

XX 20-SEP-1995 (first entry)

XX Chimeric antibody 3B9 heavy chain.

XX Chimeric antibody; antibody engineering; monoclonal antibody;
KW MAB; interleukin-4; IL-4; allergy.

XX Homo sapiens; Mus sp.

XX Key Location/Qualifiers

XX Peptide 1..19

XX /label= Sig_peptide

XX Region 51..57

XX /label= CDR

XX /note= "complementarity determining region"

XX Region 72..87

XX /label= CDR

XX /note= "complementarity determining region"

XX Peptide 120..130

XX /label= CDR

XX /note= "complementarity determining region"

XX WO9507301-A1.

XX 16-MAR-1995.

XX 07-SEP-1994; 94WO-US10308.

XX 07-SEP-1993; 93US-0117366.

XX 14-OCT-1993; 93US-0136783.

XX (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX Gross MS, Holmes SD, Sylvester DR;
 PI WPI; 1995-123387/16.
 DR N-PSDB; AAQ83492.
 XX Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
 PT from high affinity mAbs - useful in treatment of IL-4-mediated
 PT and IgE-mediated allergic conditions
 XX Disclosure; Fig.3; 97pp; English.
 PS A human/mouse chimeric antibody heavy chain variable region was
 CC constructed (given in AAR70191) that contained the mouse anti-human
 CC IL-4 MAB 3B9 variable region including 3 CDRs (AAR70199-200) and a
 CC human antibody signal peptide (AAR70193). The construct was used
 CC for humanised antibody production.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 141 AA;
 SQ Query Match 89.9%; Score 569; DB 16; Length 141;
 Best Local Similarity 90.1%; Pred. No. 1.8e-48;
 Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 QY 1 QVTLKESGPGILOPSTLSLTCSFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 60
 DB 21 QVTLKESGPGILOPSTLSLTCSFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 80
 QY 61 YNPSLKSLRTISKDTSSNOVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQGTSTVTS 120
 DB 81 YNPSLKSLRTISKDTSSNOVFLKITSVDTRDTATYYCARRVTFVYFVWVGAGITVTVS 140
 QY 121 S 121
 DB 141 S 141
 RESULT 6
 AAY23769
 ID AAY23769 standard; Protein; 141 AA.
 XX AAY23769;
 AC AAY23769;
 DT 13-SEP-1999 (first entry)
 XX Heavy chain variable region of murine/human chimeric antibody 3B9.
 DE Heavy chain variable region; interleukin-4; IL-4; antibody 3B9;
 KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;
 KW Immunoglobulin E-mediated allergic reaction; allergic rhinitis;
 KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
 KW rheumatoid arthritis; host-versus-graft disease; renal disease;
 KW allergy.
 XX Chimeric - Mus sp.
 OS Chimeric - Homo sapiens.
 XX US928904-A.
 PN 27-JUL-1999.
 PD 07-JUN-1995; 95US-0483632.
 XX 07-JUN-1995; 95US-0483632.
 XX 07-SEP-1993; 93US-0117366.
 PR 14-OCT-1993; 93US-0136783.
 PR 07-SEP-1994; 94WO-US10308.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX Gross MS, Holmes SD, Sylvester DR;
 PI WPI; 1999-429500/36.
 DR N-PSDB; AAX85886.
 XX New DNA molecules encoding recombinant antibodies useful for
 PT treating IL4-mediated conditions
 PT Example 3; Fig 3; 50pp; English.
 PS The present sequence represents the heavy chain variable region of
 CC murine/human interleukin-4 (IL-4) chimeric antibody 3B9. The
 CC specification describes chimeric and humanised IL-4 monoclonal
 CC antibodies. The antibodies of the invention are used in therapeutic
 CC and pharmaceutical compositions for treating IL-4 mediated and
 CC immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis,
 CC conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock,
 CC rheumatoid arthritis, host-versus-graft disease and renal disease.
 CC They are also useful in the diagnosis of an allergy or condition
 CC associated with excess IL-4 production through the measurement e.g. by
 CC ELISA of circulating endogenous IL-4 levels in humans.
 XX Sequence 141 AA;
 SQ Query Match 89.9%; Score 569; DB 20; Length 141;
 Best Local Similarity 90.1%; Pred. No. 1.8e-48;
 Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 QY 1 QVTLKESGPGILOPSTLSLTCSFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 60
 DB 21 QVTLKESGPGILOPSTLSLTCSFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 80
 QY 61 YNPSLKSLRTISKDTSSNOVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQGTSTVTS 120
 DB 81 YNPSLKSLRTISKDTSSNOVFLKITSVDTRDTATYYCARRVTFVYFVWVGAGITVTVS 140
 QY 121 S 121
 DB 141 S 141
 RESULT 7
 AAY18125
 ID AAY18125 standard; Protein; 141 AA.
 XX AAY18125;
 AC AAY18125;
 DT 11-AUG-1999 (first entry)
 XX Chimeric 3B9 monoclonal antibody heavy chain.
 DE Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease;
 KW allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;
 KW atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;
 KW autoimmune disease; graft versus host disease.
 XX Synthetic.
 OS US5914110-A.
 PN 22-JUN-1999.
 PD 07-JUN-1995; 95US-0483636.
 XX 07-JUN-1995; 95US-0483636.
 XX 07-SEP-1993; 93US-0117366.
 PR 14-OCT-1993; 93US-0136783.
 PR 07-SEP-1994; 94WO-US10308.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX Gross MS, Holmes SD, Sylvester DR;
 PI WPI; 1999-429500/36.
 DR N-PSDB; AAX85886.
 XX New DNA molecules encoding recombinant antibodies useful for
 PT treating IL4-mediated conditions
 PT Example 3; Fig 3; 50pp; English.
 PS The present sequence represents the heavy chain variable region of
 CC murine/human interleukin-4 (IL-4) chimeric antibody 3B9. The
 CC specification describes chimeric and humanised IL-4 monoclonal
 CC antibodies. The antibodies of the invention are used in therapeutic
 CC and pharmaceutical compositions for treating IL-4 mediated and
 CC immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis,
 CC conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock,
 CC rheumatoid arthritis, host-versus-graft disease and renal disease.
 CC They are also useful in the diagnosis of an allergy or condition
 CC associated with excess IL-4 production through the measurement e.g. by
 CC ELISA of circulating endogenous IL-4 levels in humans.
 XX Sequence 141 AA;
 SQ Query Match 89.9%; Score 569; DB 20; Length 141;
 Best Local Similarity 90.1%; Pred. No. 1.8e-48;
 Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 QY 1 QVTLKESGPGILOPSTLSLTCSFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 60
 DB 21 QVTLKESGPGILOPSTLSLTCSFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 80
 QY 61 YNPSLKSLRTISKDTSSNOVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQGTSTVTS 120
 DB 81 YNPSLKSLRTISKDTSSNOVFLKITSVDTRDTATYYCARRVTFVYFVWVGAGITVTVS 140
 QY 121 S 121
 DB 141 S 141

XX WPI; 1999-370482/31.
 DR N-PSDB; AAX79542.
 XX Recombinant IL4 antibodies
 XX Example 5; Fig 3; 50pp; English.
 XX This sequence represents the light chain of the chimeric
 CC 3B9 antibody of the invention. The antibody is a chimeric or
 CC humanised interleukin-4 (IL4) monoclonal antibody for the treatment of
 CC immunoglobulin E (IgE) mediated diseases. The antibodies are useful for
 CC the treatment of allergic disorders such as allergic rhinitis,
 CC conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock.
 CC The antibodies are also useful for regulating B and T cell proliferation
 CC and as such are useful in the treatment of autoimmune diseases and graft
 CC versus host disease.
 XX Sequence 141 AA;
 SQ Query Match 89.9%; Score 569; DB 20; Length 141;
 Best Local Similarity 90.1%; Pred. No. 1.8e-48;
 Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 QY 1 QVTLKESGPGILOPSQTLISLTCSPGFSLSLSTSGVSWIRQPSGKGLEWLAHIYWDGDKR 60
 DB 21 QVTLKESGPGILOPSQTLISLTCSPGFSLSLSTSGVSWIRQPSGKGLEWLAHIYWDGDKR 80
 QY 61 YNPSLKSLRTISKDTSSNQVFLKITSVDTTRDTATYTCARRVSLTAYAMDYWGQTSVTVS 120
 DB 81 YNPSLKSLRTISKDTSSNQVFLKITSVDTTRDTATYTCARRVTFYVYFVDMVGAGITVTVS 140
 QY 121 S 121
 DB 141 S 141
 RESULT 8
 AARS58612
 ID AARS58612 standard; Protein; 246 AA.
 XX AARS58612;
 AC AARS58612;
 XX 25-MAR-2003 (updated)
 DT 28-APR-1995 (first entry)
 DE IL-6 binding inhibitor.
 XX Human interleukin-6 binding inhibitor; IL-6; rheumatoid arthritis;
 KW septic shock; multiple myeloma; ss.
 XX Homo sapiens.
 OS EP617126-A2.
 XX 28-SEP-1994.
 PD 16-FEB-1994; 94EP-0102346.
 XX 17-FEB-1993; 93JP-0028173.
 PR (AJIN) AJINOMOTO KK.
 XX Hamuro J, Nakazawa H, Shimamura T;
 PI WPI; 1994-295777/37.
 DR N-PSDB; AAQ70612.
 XX Polypeptide inhibiting binding of human interleukin-6 (IL-6) to
 PT its receptor - useful for treating auto:immune disease induced
 PT or aggravated by IL-6
 XX Claim 5; Page 18; 26pp; English.

XX AAQ70612 codes for human interleukin-6 binding inhibitor, the
 CC polypeptide described in AARS58612. This polypeptide inhibits the
 CC binding of human IL-6 to its receptor, and can therefore be
 CC useful in the treatment of a variety of autoimmune diseases;
 CC specifically in the treatment of rheumatoid arthritis, septic
 CC shock due to bacterial infection and multiple myeloma.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 246 AA;
 SQ Query Match 89.7%; Score 567.5; DB 15; Length 246;
 Best Local Similarity 89.6%; Pred. No. 4.9e-48;
 Matches 112; Conservative 3; Mismatches 5; Indels 5; Gaps 2;
 QY 1 QVTLKESGPGILOPSQTLISLTCSPGFSLSLSTSGVSWIRQPSGKGLEWLAHIYWDGDKR 60
 DB 123 QVTLKESGPGILOPSQTLISLTCSPGFSLSLSTSGVSWIRQPSGKGLEWLAHIYWDGDKH 182
 QY 61 YNPSLKSLRTISKDTSSNQVFLKITSVDTTRDTATYTCARRVSLTA----YAMDYWGQTS 116
 DB 183 YNPSLKSLRTISKDTSSNQVFLKITSVDTTRDTATYTCARR-SLYGNWGDYAMDYWGQTS 241
 QY 117 VTSS 121
 DB 242 VTSS 246
 RESULT 9
 ABG76934
 ID ABG76934 standard; Protein; 142 AA.
 XX ABG76934;
 AC ABG76934;
 DT 05-NOV-2002 (first entry)
 DE Mouse 10D5 VH protein.
 KW Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC;
 KW variable region complementarity determining region; 3D6; 10D5;
 KW variable framework region; amyloidogenic disease; Alzheimer's disease;
 KW amyloid deposit; variable light chain; VL; variable heavy chain; VH;
 KW nototropic; neuroprotective; inhibitor of beta amyloid accumulation;
 KW Abeta.
 XX Mus musculus.
 OS WO200246237-A2.
 PN 13-JUN-2002.
 PD 06-DEC-2001; 2001WO-US46587.
 PF 06-DEC-2000; 2000US-251892P.
 PR (NEUR-) NEURALAB LTD.
 PA (AMHP) WYETH.
 XX Basi G, Saldanha J, Yednock T;
 PI WPI; 2002-519658/55.
 DR N-PSDB; ABS59429.
 XX Novel light/heavy chain of humanized immunoglobulin for treating
 PT amyloidogenic disease, has 3D6/10D5 variable region complementarity
 PT determining regions and variable framework region from human acceptor
 PT immunoglobulin -
 XX Claim 142; Figure 10; 171pp; English.
 PS The present invention relates to new humanized immunoglobulin (Ig) light
 CC chain (LC) or heavy chain (HC) comprising variable region complementarity
 CC determining regions from 3D6/10D5 Ig LC or HC variable region sequence,

CC and variable framework region from human acceptor Ig LC or HC sequence.
 CC The invention is useful for preventing or treating an amyloidogenic
 CC disease or Alzheimer's disease in a patient. The invention is also useful
 CC for in vivo imaging amyloid deposits in a patient. The present amino
 CC acid sequence represents a mouse 3D6/10D5 variable light (VL) chain or
 CC variable heavy (VH) chain protein of the invention.

XX
 SQ Sequence 142 AA;
 Query Match 87.0%; Score 551; DB 23; Length 142;
 Best Local Similarity 87.8%; Pred. NO. 1.1e-46;
 Matches 108; Conservative 1; Mismatches 12; Indels 2; Gaps 1;
 QY 1 QVTLKESGPGIILQPSQTLTLTCSFSGFSLSTSGMGVSWIRQPSGKLEWLAHIYWDGDKR 60
 Db 20 QATLKESGPGIILQSSQTLTLTCSFSGFSLSTSGMGVSWIRQPSGKLEWLAHIYWDGDKR 79
 QY 61 YNPSLKSRLLTISKDTSSNOVFLKITSVDTRDTATYYCARR--VSLTAYAMDYWGQGTSTV 118
 Db 80 YNPSLKSRLLTISKDTSRKQVFLKITSVDPADTATYYCVRPITPVLVDAMDYWGQGTSTV 139
 QY 119 VSS 121
 Db 140 VSS 142

RESULT 10
 AAR54101
 ID AAR54101 standard; Protein; 122 AA.
 XX
 AC AAR54101;
 XX
 DT 08-FEB-1995 (first entry)
 XX
 DE Humanised MAb H-chain.
 XX
 KW Human; murine; heavy; light; chain; monoclonal; antibody;
 KW complementarity determining region; CDR; IgG; kappa; IIIB; IIIM.
 XX
 OS Chimeric - Mus musculus.
 OS Chimeric - Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 31..37
 FT /label= CDR1
 FT Region 52..67
 FT /label= CDR2
 FT Region 100..111
 FT /label= CDR3

XX JP06141885-A.
 XX
 XX
 PD 24-MAY-1994.
 XX
 PF 05-NOV-1992; 92JP-0322476.
 XX
 PR 05-NOV-1992; 92JP-0322476.
 XX
 XX (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
 XX
 XX WPI; 1994-205040/25.
 DR N-PSDB; AAQ68709.

XX Recombinant anti-HIV monoclonal antibody - capable of
 XX neutralising strains which can not be neutralised by anti-IIIB
 XX and IIIMN antibodies
 XX
 PS Disclosure; Page 13; 23pp; Japanese.
 XX
 XX The sequences given in AAR54101-02 represent the heavy and light chains
 CC respectively of the humanised monoclonal antibody (MAb) of the
 CC invention. The antibody has the ability to neutralise human
 CC immunodeficiency virus. The antibody is classified as IgG kappa and

CC has the sequence RIGPCR or RVGPCR in the principal neutralising
 CC domain. The antibody may be used to neutralise the clinically
 CC separate strains which cannot be neutralised by the neutralising
 CC antibodies against IIIB and IIIMN strains.

XX
 SQ Sequence 122 AA;
 Query Match 86.3%; Score 546.5; DB 15; Length 122;
 Best Local Similarity 87.7%; Pred. NO. 2.5e-46;
 Matches 107; Conservative 5; Mismatches 9; Indels 1; Gaps 1;
 QY 1 QVTLKESGPGIILQPSQTLTLTCSFSGFSLSTSGMGVSWIRQPSGKLEWLAHIYWDGDKR 60
 Db 1 QVTLKESGPGIILQPSQTLTLTCSFSGFSLSTSGMGVSWIRQPSGKLEWLAHIYWDGDKR 60
 QY 61 YNPSLKSRLLTISKDTSSNOVFLKITSVDTRDTATYYCARRVSL-TAYAMDYWGQGTSTV 119
 Db 61 YNPSLKSRLLTISEDTSSNOVFLKITTVDTADTATYYCARRVFGNSDFDHWGQGTSTV 120
 QY 120 SS 121
 Db 121 SS 122

RESULT 11
 AAR88109
 ID AAR88109 standard; peptide; 120 AA.
 XX
 AC AAR88109;
 XX
 DT 25-JUL-1996 (first entry)
 XX
 DE Murine anti-Protein C MAb HPC-4 VH gamma mature peptide.
 XX
 KW Epitope; activation; heavy chain; protein C; vitamin K; plasma protein;
 KW zymogen; cleavage; mouse; humanised antibody; variable region;
 KW light chain; inhibition; anticoagulant; coagulation; tumour.
 XX
 OS Mus musculus.
 XX
 FN WO9534652-A1.
 XX
 PD 21-DEC-1995.
 XX
 PF 09-JUN-1995; 95WO-US07372.
 XX
 PR 10-JUN-1994; 94US-0259321.
 XX
 PA (OKLA-) OKLAHOMA MED RES FOUND.
 XX
 PI Esmon CT, Rezaie A;
 XX
 DR WPI; 1996-049681/05.
 DR N-PSDB; AAT09300.
 XX
 PT Calcium-binding monoclonal antibody immunoreactive with Protein C -
 PT inhibits Protein C anticoagulant activation by
 PT thrombin-thrombomodulin, e.g. for treating tumours
 XX
 PS Claim 2; Page 29; 41pp; English.

XX This is the amino acid sequence of the mature peptide from the murine
 CC anti-protein C monoclonal antibody HPC-4 heavy chain variable region.
 CC HPC-4 recognises the activation peptide region (AAR88106) of the heavy
 CC chain of protein C, a vitamin K-dependent plasma protein zymogen.
 CC Protein C is converted to activated protein C (APC) by cleavage between
 CC the Arg-Leu amino acid contained within the activation peptide sequence.
 CC HPC-4 prevents protein C activation to APC by binding to this region.
 CC The DNA sequences encoding the variable regions of the heavy and light
 CC chains of the antibody (AAT09299-302) were used to construct humanised
 CC antibodies using the PCR primers AAT09303-9. The humanised antibodies
 CC are useful as inhibitors of coagulation and can be used for the treatment
 CC of tumours by inhibiting the anticoagulant activity of APC by preventing

CC conversion of protein C to APC.

XX Sequence 120 AA;

Query Match 82.5%; Score 522.5; DB 17; Length 120;
Best Local Similarity 84.3%; Pred. No. 5.8e-44;
Matches 102; Conservative 3; Mismatches 15; Indels 1; Gaps 1;

QY 1 QVTLKESGPGILOPQSOTLSTCSFSGFSLSTSGMGVSWIRQPSGKGLWLAHIYWDGDKR 60

Db 1 QVTLKESGPGILOPQSOTLSTCSFSGFSLSTSGMGVSWIRQPSGKGLWLAHIYWDGDKR 60

QY 61 YNPSLKSRLLTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQTSVTVS 120

Db 61 YNPSLKSRLLTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQTSVTVS 119

QY 121 S 121

Db 120 S 120

RESULT 12

AAR88107
ID AAR88107 standard; Protein; 139 AA.

XX AAR88107;

DT 25-JUL-1996 (first entry)

XX Murine anti-Protein C MAb HPC-4 VH gamma protein.

XX Epitope; activation; heavy chain; protein C; vitamin K; plasma protein;
KW zymogen; cleavage; mouse; humanised antibody; variable region;
KW light chain; inhibition; anticoagulant; coagulation; tumour.

XX Mus musculus.

XX Key Location/Qualifiers
FH Peptide 1..19
FT /note= "signal peptide"

FT Peptide 20..139
FT /note= "mature peptide"

XX W09534652-A1.

XX 21-DEC-1995.

XX 09-JUN-1995; 95WO-US07372.

XX 10-JUN-1994; 94US-0259321.

XX (OKLA-) OKLAHOMA MED RES FOUND.

XX Esmon CT, Rezaie A;

XX WPI; 1996-049681/05.

DR N-PSDB; AAT09299.

XX Calcium-binding monoclonal antibody immunoreactive with Protein C -
PT inhibits Protein C anticoagulant activation by
PT thrombin-thrombomodulin, e.g. for treating tumours

PS Claim 2; Page 29; 4lpp; English.

XX This is the amino acid sequence of the heavy chain variable region from
CC the murine anti-protein C monoclonal antibody HPC-4 which recognises
CC the activation peptide region (AAR88106) of the heavy chain of protein
CC C, a vitamin K-dependent plasma protein zymogen. Protein C is converted
CC to activated protein C (APC) by cleavage between the Arg-Leu amino acid
CC contained within the activation peptide sequence. HPC-4 prevents
CC protein C activation to APC by binding to this region. The DNA sequences
CC encoding the variable regions of the heavy and light chains of the
CC antibody (AAT09299-302) were used to construct humanised antibodies using

CC the PCR primers AAT09303-9. The humanised antibodies are useful as
CC inhibitors of coagulation and can be used for the treatment of tumours by
CC inhibiting the anticoagulant activity of APC by preventing conversion of
CC protein C to APC.

XX Sequence 139 AA;

Query Match 82.5%; Score 522.5; DB 17; Length 139;
Best Local Similarity 84.3%; Pred. No. 6.9e-44;
Matches 102; Conservative 3; Mismatches 15; Indels 1; Gaps 1;

QY 1 QVTLKESGPGILOPQSOTLSTCSFSGFSLSTSGMGVSWIRQPSGKGLWLAHIYWDGDKR 60

Db 20 QVTLKESGPGILOPQSOTLSTCSFSGFSLSTSGMGVSWIRQPSGKGLWLAHIYWDGDKR 79

QY 61 YNPSLKSRLLTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQTSVTVS 120

Db 80 YNPSLKSRLLTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQTSVTVS 138

QY 121 S 121

Db 139 S 139

RESULT 13

AAR67655
ID AAR67655 standard; Protein; 139 AA.

XX AAR67655;

DT 25-MAR-2003 (updated)

DT 21-AUG-1995 (first entry)

XX Mouse heavy chain variable region amino acid sequence.

XX Primer; PCR; amplify; kappa; light chain; variable region; mouse; human;
KW interleukin; antibody; hybridoma; CDR; framework; constant region;
KW heavy chain; disorder; antigenicity.

XX Synthetic.

XX Key Location/Qualifiers
FH Peptide 1..19
FT /label= signal peptide

FT Peptide 20..139
FT /label= mature peptide

XX W09428159-A1.

XX 08-DEC-1994.

XX 30-MAY-1994; 94WO-JPC0859.

XX 31-MAY-1993; 93JP-0129787.

XX (CHUS) CHUGAI SEIYAKU KK.

XX (CHUS) CHUGAI PHARM CO LTD.

XX Hirata Y, Sato K, Tsuchiya M;

XX WPI; 1995-022828/03.

DR N-ESDB; AAQ75889.

XX Antibody against IL-6 - useful for the therapy and treatment of

PT IL-6 related disorders.

XX Claim 10; Page 49; 82pp; Japanese.

XX The deduced amino acid sequence of the heavy chain variable region of
CC the mouse anti-human interleukin-6 (IL-6) antibody. The gene was
CC amplified by primers (AA075876-87) from cDNA derived from mRNA from
CC mouse SK2 hybridoma cells. The fragment was cloned into plasmid pUC19
CC to produce plasmid pUC-SK2-Vh. The inserted fragment is used to

CC generate constructs (see AAQ75914-7) encoding fragments of an antibody to
 CC the human IL-6 comprising (a) a light chain with (i) a variable region
 CC containing 3 complementarity determining regions (CDR) (AAR77201-3)
 CC inserted into several framework regions (FR) (AAR77204-7) and (ii) a human
 CC light chain constant region and (b) a heavy chain with (i) a variable
 CC region containing 3 CDR (AAR77212-4) inserted into an FR (AAR77215-8) and
 CC (ii) a human light chain constant region. The FR of the light chain may
 CC be mouse derived (AAQ75888) or from the human antibody RE1. The heavy
 CC chain FR may also be mouse derived (AAQ75889) or from the human antibody
 CC DAW. The antibodies can be used in the treatment of IL-6 related
 CC disorders. The antibodies are useful as they have low antigenicity due to
 CC the use of human derived sequences and low antigenicity mouse derived
 CC sequences.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 139 AA;
 Query Match 82.4%; Score 521.5; DB 16; Length 139;
 Best Local Similarity 83.7%; Pred. No. 8.7e-44;
 Matches 103; Conservative 6; Mismatches 9; Indels 5; Gaps 2;
 QY 1 QVTLKESGPGIQLPSQTLTLTCSFGSFLSTSGMGVSWIRQPSGKGLEWLAHIYWDDBDKR 60
 DB 20 QVTLKESGPGIQLPSQTLTLTCSFGSFLSTSGMTVGWIRQPSGKGLEWLAHIWNNDDKY 79
 QY 61 YNPPLKSLRLTISKDTSSNOVFLKITSVDTRDTATYYCARRVSLTAY--AMDYWGQGTSTV 118
 DB 80 YNPPLKSLRLTISKDTSSNOVFLKITSVDTRDTATYYCAR---WEDYDEAMDYWGQGTSTV 136
 QY 119 VSS 121
 DB 137 VSS 139

RESULT 14
 ABG67188
 ID ABG67188 standard; Protein; 121 AA.
 XX AC ABG67188;
 XX DT 24-SEP-2002 (first entry)
 XX DE Human IgG1 antibody heavy chain variable region 15H4VH.
 XX KW Hepatitis C virus vaccine; HCV; hypervariable region 1; HVR1;
 XX KW envelope protein E2; antibody; helper T-lymphocyte; IgG1;
 XX KW cytotoxic T-lymphocyte; HCV infection; virucide; heavy chain.
 XX OS Homo sapiens.

XX WO200245743-A2.
 XX 13-JUN-2002.
 XX PF 07-DEC-2001; 2001WO-GB05421.
 XX PR 09-DEC-2000; 2000GB-0030102.
 XX PR 18-DEC-2000; 2000GB-0030789.
 XX PA (ALLA/) ALLAIN J.
 XX PI Allain J, Li C, Piccolella E;
 XX WPI; 2002-508540/54.
 XX DR Hepatitis C virus (HCV) vaccines able to raise antibodies, helper T
 XX PT lymphocytes and/or cytotoxic T lymphocytes able to bind to the
 XX PT hypervariable 1 region of the infecting HCV strain -
 XX Example 4; Fig 2; 52pp; English.

XX The present invention relates to a hepatitis C virus (HCV) vaccine
 CC comprising different groups of peptides each group being capable of

CC raising, in an infected individual, an antibody able to bind to the
 CC hypervariable 1 (HVR1) region of the envelope protein E2 of the
 CC infecting HCV strain. The different groups of peptides are
 CC administered sequentially to raise antibodies, helper T-lymphocytes,
 CC and cytotoxic T-lymphocytes which are cross-reactive to the HVR1
 CC region of the infecting HCV. The vaccines are useful for preventing
 CC and treating chronic HCV infections. ABG67188-ABG67189 represent
 CC variable regions of human IgG1 antibody heavy chain.

XX SQ Sequence 121 AA;
 Query Match 82.1%; Score 520; DB 23; Length 121;
 Best Local Similarity 85.2%; Pred. No. 1e-43;
 Matches 104; Conservative 7; Mismatches 7; Indels 4; Gaps 3;
 QY 1 QVTLKESGPGIQLPSQTLTLTCSFGSFLSTSGMGVSWIRQPSGKGLEWLAHIY-WDDDK 59
 DB 1 QVTLKESGPGIQLPSQTLTLTCSFGSFLSTSGMGVSWIRQPSGKGLDLWLAHIYPWDDDK 60
 QY 60 RYNPLKSLRLTISKDTSSNOVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQGTSTV 119
 DB 61 RYNPLKSLRLTISKDTSSNOVFLKITSVDTRDTATYYCAQIIT-TWFA--HWGQGLTIV 117
 QY 120 SS 121
 DB 118 SS 119

RESULT 15
 AAY25396
 ID AAY25396 standard; Protein; 121 AA.
 XX AC AAY25396;
 XX DT 07-SEP-1999 (first entry)
 XX DE WO9932630 Seq ID 35.
 XX KW Paraquat; antibody; light chain; herbicide; resistant; crop plant;
 XX KW weed control; tolerant; diquat; photosynthesis inhibitor; photosystem I;
 XX KW free radical; lipid peroxidation; electron transport; photosystem II;
 XX KW vacuole; cell surface; cytotoxic; sensitive.

XX OS Unidentified.
 XX PN WO9932630-A1.
 XX PD 01-JUL-1999.
 XX PF 15-DEC-1998; 98WO-GB03760.
 XX PR 19-DEC-1997; 97GB-0026955.
 XX PA (ZENE) ZENECA LTD.
 XX PI Holt DC, Jones PG;
 XX WPI; 1999-405173/34.
 XX PT Herbicide binding proteins and related polynucleotides
 XX PS Disclosure; Page 43-44; 60pp; English.

XX This invention describes a novel herbicide binding protein which can
 CC confer herbicide resistance activity. Crop plants, such as soybean,
 CC cotton, tobacco, sugarbeet, oilseed rape, canola, flax, sunflower,
 CC potato, tomato, alfalfa, lettuce, maize, wheat, sorghum, rye, bananas,
 CC barley, oat, turf grass, forage grass, sugar cane, pea, field bean,
 CC rice, pine, poplar, apple, grape, citrus or nut plants, transformed
 CC with a herbicide binding protein gene are resistant to the herbicide.
 CC Hence, weeds can be selectively controlled in a field of the transformed
 CC crops. The plants are substantially resistant or tolerant to herbicides,
 CC such as paraquat or diquat, that inhibit photosynthesis by accepting

Search completed: January 14, 2004, 19:11:24
Job time : 40.1905 secs

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OM protein - protein search, using sw model

Run on: January 14, 2004, 19:02:07 ; Search time 16.2381 Seconds
(without alignments)
716.612 Million cell updates/sec

Title: US-09-759-112A-7
Perfect score: 633
Sequence: 1 QVTLKESGPGILQPSQTLSL.....SLTAYAMYWGQGSVTVSS 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:.*
1: PIR1:.*
2: PIR2:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	551.5	87.1	122	2 S11740	Ig heavy chain pre
2	543.5	85.9	143	2 PT0174	Ig heavy chain pre
3	491	77.6	107	2 A49442	Ig heavy chain v r
4	474.5	75.0	113	2 S26465	Ig heavy chain v r
5	472.5	74.6	116	2 S26328	Ig heavy chain v r
6	471	74.4	138	2 S31513	Ig heavy chain - h
7	460	72.7	121	2 S09959	Ig heavy chain v r
8	454.5	71.8	124	2 A49002	Ig heavy chain v r
9	448	70.8	103	2 B25913	Ig heavy chain pre
10	436	68.9	374	2 S69339	Ig heavy chain v r
11	419.5	66.3	120	1 GIHUCO	Ig heavy chain v r
12	412	65.1	121	2 A36005	Ig heavy chain v r
13	410	64.8	119	2 S18555	Ig heavy chain v r
14	407	64.3	125	1 MHHUWC	Ig heavy chain v r
15	402.5	63.6	147	1 G2HUCS	Ig heavy chain pre
16	395	62.4	121	1 G1HUHE	Ig heavy chain v r
17	390.5	61.7	122	2 S20809	Ig heavy chain v r
18	384.5	60.7	120	2 FL0087	Ig heavy chain v r
19	384	60.7	144	1 G2MS14	Ig heavy chain v r
20	383.5	60.6	118	2 S18556	Ig heavy chain pre
21	382	60.3	146	2 S09711	Ig heavy chain v r
22	379.5	60.0	117	2 S38563	Ig heavy chain v r
23	377	59.6	96	2 S26924	Ig heavy chain v r
24	377	59.6	140	2 I37782	Ig variable region
25	376	59.4	147	2 S13519	Ig heavy chain v r
26	373.5	59.0	122	2 A49049	Ig heavy chain v r
27	373.5	59.0	137	2 S31676	Ig heavy chain v r
28	372	58.8	155	2 S31511	Ig heavy chain - h
29	371	58.6	96	2 S26923	Ig heavy chain v r

Ig heavy chain V r
Ig heavy chain V-I
Ig heavy chain V r
Ig heavy chain V r
Ig heavy chain - h
Ig heavy chain V r
Ig heavy chain pre
Ig heavy chain v r
gene C72-3A1 prote
Ig heavy chain V r
Ig heavy chain pre
Ig heavy chain h
Ig heavy chain V r
Ig heavy chain V r
Ig heavy chain pre
Ig heavy chain V r

ALIGNMENTS

RESULT 1

S11740
Ig heavy chain precursor V-D-J region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S11740
R:Hayakawa, K.; Carmarck, C.E.; Hyman, R.; Hardy, R.R.
submitted to the EMBL Data Library, May 1990
A:Description: Natural autoantibodies to thymocytes: Origin, VH genes, fine specificity.
A:Reference number: S11740
A:Accession: S11740
A:Molecule type: mRNA
A:Residues: 1-122 <EMB>
A:Cross-references: EMBL:X53097; NID:952368; PIDN:CAA37261.1; PID:9762983
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:22-106/Domain: immunoglobulin homology <IMM>

Query Match 87.1%; Score 551.5; DB 2; Length 122;
Best Local Similarity 91.4%; Pred. No. 3.4e-45;
Matches 106; Conservative 2; Mismatches 7; Indels 1; Gaps 1;

QY	1	QVTLKESGPGILQPSQTLSLTCSFGSLSTSGMGSVIRQPSGKGLWLAHYWDDDKR	60
Db	8	QVTLKESGPGILQPSQTLSLTCSFGSLSTSGMGSVIRQPSGKGLWLAHYWDDDKR	67
QY	61	YNPSLKRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMQVWGQTS	116
Db	68	YNPSLKRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMQVWGQTT	122

RESULT 2

PT0174
Ig heavy chain precursor V region (IDB5.7) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Aug-1996
C:Accession: PT0174
R:Perfetti, V.; Borden, P.; Tao, M.H.; Morrison, S.L.; Kabat, E.A.
Mol. Immunol. 28, 505-515, 1991
A:Title: Specificity and variable region cDNA sequence of an isogeneic monoclonal anti:
A:Reference number: PT0174; MUID:91287738; PMID:1712074
A:Accession: PT0174
A:Molecule type: mRNA
A:Residues: 1-143 <PER>
A:Experimental source: strain BALB/c
C:Comment: IDB5.7 is an antibody to anti-alpha (1-6) dextran.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-118/Domain: immunoglobulin homology <IMM>

Query Match 85.9%; Score 543.5; DB 2; Length 143;
Best Local Similarity 85.7%; Pred. No. 2.3e-44;

```
Matches 108; Conservative 2; Mismatches 9; Indels 7; Gaps 2;
QY 1 QVTLKESGPILOPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 60
Db 20 QVTLKESGPILOPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 79
QY 61 YNPSLKSLRTISKDTSSNOVFLKITSVDTRDTATYTCARRVSLTAYA-----MDYWGQGT 115
Db 80 YNPSLKSLRTISKDTSSNOVFLKITSVDTRDTATYTCARRVSLTAYA-----MDYWGQGT 137
QY 116 SVTVSS 121
Db 138 SVTVSS 143

RESULT 3
A49442
Ig heavy chain V region (50.1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C:Accession: A49442
R;Stura, E.A.; Stanfield, R.L.; Fieser, G.G.; Silver, S.; Roguska, M.; Hincapié, L.M.; S
Proteins 14, 499-508, 1992
A:Title: Crystallization, sequence, and preliminary crystallographic data for an antipep
A:Reference number: A49442; MUID:93056166; PMID:1438187
A:Accession: A49442
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-107 <STU>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-91/Domain: immunoglobulin homology <IMM>

Query Match 77.6%; Score 491; DB 2; Length 107;
Best Local Similarity 84.1%; Pred. No. 1.5e-39;
Matches 95; Conservative 4; Mismatches 8; Indels 6; Gaps 1;

QY 9 PGILQPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKRYNPSLKSR 68
Db 1 PGILQPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKRYNPSLKSR 60
QY 69 LTISKDTSSNOVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQGTSTVTVSS 121
Db 61 LKISKDTSSNOVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQGTSTVTVSS 107

RESULT 4
S26465
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S26465
R;Kavaler, J.
submitted to the EMBL Data Library, April 1991
A:Reference number: S26459
A:Accession: S26465
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <KAV>
A:Cross-references: EMBL:X59115; NID:g51928; PIDN:CAA41841.1; PID:g51929
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:6-90/Domain: immunoglobulin homology <IMM>

Query Match 75.0%; Score 474.5; DB 2; Length 113;
Best Local Similarity 81.4%; Pred. No. 5.9e-36;
Matches 92; Conservative 5; Mismatches 13; Indels 3; Gaps 1;

QY 10 GILQPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKRYNPSLKRL 69
Db 1 GILQPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKRYNPSLKRL 60
QY 70 TISKDTSSNOVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQGTSTVTV 119

Matches 108; Conservative 2; Mismatches 9; Indels 7; Gaps 2;
QY 1 QVTLKESGPILOPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 60
Db 20 QVTLKESGPILOPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 79
QY 61 YNPSLKSLRTISKDTSSNOVFLKITSVDTRDTATYTCARRVSLTAYA-----MDYWGQGT 115
Db 80 YNPSLKSLRTISKDTSSNOVFLKITSVDTRDTATYTCARRVSLTAYA-----MDYWGQGT 137
QY 116 SVTVSS 121
Db 138 SVTVSS 143

RESULT 5
S26328
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C:Accession: S26328
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protein e
A:Reference number: S26309; MUID:91341421; PMID:1908510
A:Accession: S26328
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-116 <STA>
A:Cross-references: EMBL:X59198; NID:g52074; PIDN:CAA41908.1; PID:g1334038
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:11-95/Domain: immunoglobulin homology <IMM>

Query Match 74.6%; Score 472.5; DB 2; Length 116;
Best Local Similarity 79.3%; Pred. No. 9.3e-38;
Matches 92; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

QY 6 ESGPILQPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKRYNPSL 65
Db 2 ESGPILQPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKRYNPSL 61
QY 66 KSLRTISKDTSSNOVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQGTSTVTVSS 121
Db 62 KSLRTISKDTSSNOVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQGTSTVTVSS 116

RESULT 6
S31513
Ig heavy chain - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S31513
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA aut
A:Reference number: S31509
A:Accession: S31513
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-138 <CHA>
A:Cross-references: EMBL:X69861; NID:g33084; PIDN:CAA49495.1; PID:g33085
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:30-114/Domain: immunoglobulin homology <IMM>

Query Match 74.4%; Score 471; DB 2; Length 138;
Best Local Similarity 73.0%; Pred. No. 1.6e-37;
Matches 89; Conservative 15; Mismatches 16; Indels 2; Gaps 1;

QY 1 QVTLKESGPILOPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 60
Db 16 QVTLKESGPILOPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 75
QY 61 YNPSLKSLRTISKDTSSNOVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQGTSTV 118
Db 76 YNPSLKSLRTISKDTSSNOVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQGTSTV 135
QY 119 VS 120
Db 136 VS 137

RESULT 7
```

B25913
IG heavy chain precursor V region (BFL23) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 16-Aug-1996
C:Accession: B25913
R:Lawler, A.M.; Lin, P.S.; Gearhart, P.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 2454-2458, 1987
A:Title: Adult B-cell repertoire is biased toward two heavy-chain variable-region genes
A:Reference number: A94148; MUID:87175692; PMID:3104915
A:Accession: B25913
A:Molecule type: DNA
A:Residues: 1-103 <LAW>
A:Note: the authors translated the codon TGT for residue 11 as Ser
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:19-103/Domain: immunoglobulin homology <IMM>

Query Match 70.8%; Score 448; DB 2; Length 103;
Best Local Similarity 85.9%; Pred. No. 1.7e-35;
Matches 85; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 QVTLKESGPIIQPSQTLTLTCSFSGFSISTSGMGVSWIRQPSGKGLEWLAHIYWDGDKR 60
DB 5 QVTLKECGPIIQPSQTLTLTCSFSGFSISTSGMGVSWIRQPSGKGLEWLLILWDSKY 64
QY 61 YNPISLKSRTITISKDTSSNQVFLKITSVDTRDTATYYCAR 99
DB 65 YNPALKSRITISKDTYNNQVFLKIANVDADTATYYCAR 103

RESULT 10
S69339
IG heavy chain V region precursor - human
C:Species: Homo sapiens (man)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C:Accession: S69339; S72664
R:Khamlichi, A.A.; Auccouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A:Reference number: S69339; MUID:95262687; PMID:7744049
A:Accession: S69339
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <KHA>
A:Cross-references: EMBL:X81695
R:Khamlichi, A.A.
submitted to the EMBL Data Library, September 1994
A:Reference number: S72664
A:Accession: S72664
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140, 'C', 142-374 <KH2>
A:Cross-references: EMBL:X81695
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 68.9%; Score 436; DB 2; Length 374;
Best Local Similarity 66.4%; Pred. No. 9.8e-34;
Matches 83; Conservative 17; Mismatches 19; Indels 6; Gaps 2;

QY 1 QVTLKESGPIIQPSQTLTLTCSFSGFSISTSGMGVSWIRQPSGKGLEWLAHIYWDGDKR 60
DB 20 QVTLKESGPIIVKPTLTTLTTFSGFSLSKSGVGWIRQPPGQALEWLAHIFWDDDKR 79
QY 61 YNPISLKSRTITISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAYAMDY---WGQGTS 116
DB 80 YSPSLRTRLTITIKDTSKNQVLTMTNVDPADTATYYCG--YSVEGYGGYRHSWGQGLT 137
QY 117 VTVSS 121
DB 138 VTVSS 142

RESULT 11

GIHUCO

IG heavy chain V-II region (Cor) - human (tentative sequence)
C:Species: Homo sapiens (man)
C:Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 31-Mar-2000
C:Accession: A02089
R:Press, E.M.; Hogg, N.M.
Biochem. J. 117, 641-660, 1970
A:Title: The amino acid sequences of the Fd fragments of two human gamma heavy chains.
A:Reference number: A90250; MUID:70258837; PMID:5449120
A:Accession: A02089
A:Molecule type: protein
A:Residues: 1-120 <PRE>
C:Comment: This chain was isolated from an IgG1 myeloma protein.
C:Genetics:
A:Gene: GDB:IGHV@
A:Cross-references: GDB:128528; OMIM:147070
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein; heterotetramer; immunoglobulin; pyroglutamic acid
F:15-96/Domain: immunoglobulin homology <IMM>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:22-94/Disulfide bonds: #status experimental
F:62/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 66.3%; Score 419.5; DB 1; Length 120;
Best Local Similarity 68.3%; Pred. No. 9.9e-33;
Matches 84; Conservative 15; Mismatches 19; Indels 5; Gaps 2;
QY 1 QVTLKESGPGILQPSQTLSTCSFSGSLSTSGMGVSWIRQPSGKLEWLAHYWDDDKR 60
DB 1 QVTLRESGPAVKPTQTLTCTCTFSGFSLSTGMCVGVWIRQPPGKLEWLAHYWDDDKY 60
QY 61 YNPSLKSRITISKDTSSNOVFLKITSVDTRDTATYTCARVSLTAY--MDYWGQTSVT 118
DB 61 YNTSLKTRITISKDTSSNOVFLKITSVDTRDTATYTCARVSLTAY--MDYWGQTSVT 117
QY 119 VSS 121
DB 118 VSS 120

RESULT 12

A36005
IG heavy chain V region (M60) - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1990 #sequence_revision 13-Sep-1991 #text_change 16-Dec-1998
C:Accession: A36005
R:Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150; 1990
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A:Reference number: A36005; MUID:90349571; PMID:2117273
A:Accession: A36005
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-121 <SCH>
A:Cross-references: GB:M34027
C:Genetics:
A:Gene: GDB:IGHV1
A:Cross-references: GDB:118731; OMIM:146910
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 65.1%; Score 412; DB 2; Length 121;
Best Local Similarity 66.9%; Pred. No. 5.1e-32;
Matches 81; Conservative 15; Mismatches 25; Indels 0; Gaps 0;
QY 1 QVTLKESGPGILQPSQTLSTCSFSGSLSTSGMGVSWIRQPSGKLEWLAHYWDDDKR 60
DB 1 EVTLRESGPAVKPTQTLTCTCTYGFSLSTSGMCVSWIRQPPGKLEWLAHYWDDDKY 60
QY 61 YNPSLKSRITISKDTSSNOVFLKITSVDTRDTATYTCARVSLTAYMDYWGQTSVT 120

Db 61 YSTSLKTRITISKDTSKNQVLTMTNMDPVDATYTCARINNMGEGYFDLWGRGTLVTVS 120
QY 121 S 121
Db 121 S 121

RESULT 13

S18555
IG heavy chain V region precursor (VII-5) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 21-Jul-2000
C:Accession: S18555
R:Shin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; F
EMBO J. 10, 3641-3645, 1991
A:Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cl
A:Reference number: S18551; MUID:92037524; PMID:1935893
A:Accession: S18555
A:Molecule type: DNA
A:Residues: 1-119 <SHI>
A:Cross-references: EMBL:X62111; NID:g37839; PIDN:CAA44021.1; PID:g3980125
C:Genetics:
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-119/Product: Ig heavy chain V region (VII-5) #status predicted <MAT>
F:34-118/Domain: immunoglobulin homology <IMM>

Query Match 64.8%; Score 410; DB 2; Length 119;
Best Local Similarity 75.0%; Pred. No. 7.7e-32;
Matches 75; Conservative 14; Mismatches 11; Indels 0; Gaps 0;
QY 1 QVTLKESGPGILQPSQTLSTCSFSGSLSTSGMGVSWIRQPSGKLEWLAHYWDDDKR 60
DB 20 QITLKESGPTLVKPTQTLTCTCTFSGFSLSTSGVGVWIRQPPGKALEWLAHYWDDDKR 79
QY 61 YNPSLKSRITISKDTSSNOVFLKITSVDTRDTATYTCAR 100
DB 80 YSPSLKSRITITKDTSKNQVLTMTNMDPVDATYTCAR 119

RESULT 14

MEHLWC
IG heavy chain V-II region (MCE) - human
C:Species: Homo sapiens (man)
C:Date: 14-Nov-1983 #sequence_revision 22-Nov-1983 #text_change 02-Sep-1997
C:Accession: A02092
R:Gerber-Jenson, B.; Kazin, A.; Kehoe, J.M.; Scheffel, C.; Erickson, B.W.; Litman, G.W.
J. Immunol. 126, 1212-1216, 1981
A:Title: Molecular basis for the temperature-dependent insolubility of cryoglobulins. X
A:Reference number: A02092; MUID:8118242; PMID:6780622
A:Accession: A02092
A:Molecule type: protein
A:Residues: 1-125 <GER>
A:Note: This chain was derived from a monoclonal IgM cryoimmunoglobulin
C:Genetics:
A:Gene: GDB:IGHV@
A:Cross-references: GDB:128528; OMIM:147070
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin; pyroglutamic acid
F:15-99/Domain: immunoglobulin homology <IMM>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 64.3%; Score 407; DB 1; Length 125;
Best Local Similarity 63.2%; Pred. No. 1.6e-31;
Matches 79; Conservative 17; Mismatches 25; Indels 4; Gaps 1;
QY 1 QVTLKESGPGILQPSQTLSTCSFSGSLSTSGMGVSWIRQPSGKLEWLAHYWDDDKR 60
DB 1 QITLKESGPTLVKPTQTLTCTCTFSGFSLSTSGVGVWIRQPPGKALEWLAHYWDDDKR 60


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QY 61 YNPSLKSRLTISKDTSSNQVFLKITSVDRDTATYYCAR-----RVSLTAYAMYWGQGTS 116
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 YSPSLASRLTGTGRNQVLTITNMDPVDSGTFCARHPWPWFCTGNLGGFDXWGQGT 120
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 117 VTVSS 121
      |||||
Db 121 VTVSS 125
      |||||

RESULT 15
G2HUCS
IG heavy chain precursor V-II region (Cess) - human
C/Species: Homo sapiens (man)
C/Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 02-Sep-1997
C/Accession: A02090
R/Takahashi, N.; Noma, T.; Honjo, T.
Proc. Natl. Acad. Sci. U.S.A. 81, 5194-5198, 1984
A/Title: Rearranged immunoglobulin heavy chain variable region (V-H) pseudogene that del
A/Reference number: A02090; MUID:84298107; PMID:6069186
A/Accession: A02090
A/Molecule type: mRNA
A/Residues: 1-147 <TAK>
A/Note: the sequence was determined from the differentiated gene
A/Note: the authors translated the codon GGG for residue 16 as Trp, TGC for residue 142
as Ser, and CAG for residue 147 as Ser
C/Genetics:
A/Gene: GDB:IGHV@
A/Cross-references: GDB:128528; OMIM:147070
A/Map position: 14q32.33-14q32.33
A/Introns: 15/3
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/1-19/Domain: signal sequence #status predicted <SIG>
F/20-147/Product: Ig heavy chain V-II region (Cess) #status predicted <MAT>
F/20-118/Region: V segment
F/34-118/Domain: immunoglobulin homology <IMM>
F/119-132/Region: D segment
F/133-147/Region: J segment

Query Match 63.6%; Score 402.5; DB 1; Length 147;
Best Local Similarity 62.3%; Pred. No. 5e-31;
Matches 76; Conservative 16; Mismatches 23; Indels 7; Gaps 1;

QY 1 QVTLKESGPGIQLPSQTLISLTSFSGFSLSTSGMGVSWIRQPSGKGLWLAHIYWDDEKR 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 QVNLRESGPALVXATHLTITCTFSGLSVNTRCMSVSWIRQPPGKALEWLARIDWDDKY 79'
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 YNPSLKSRLTISKDTSSNQVFLKITSVDRDTATYYCA-----RVSLTAYAMYWGQ 113
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 YGTSLETRLTISKDTSKNQVVLKVTNMDPADTATYYCARNQVMTMREVMITSNAFDIWGQ 139
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 114 GT 115
      ||
Db 140 GT 141
      ||

Search completed: January 14, 2004, 19:13:47
Job time : 17.2381 secs
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OM protein - protein search, using sw model

Run on: January 14, 2004, 17:48:21 ; Search time 11 Seconds
(without alignments)
517.294 Million cell updates/sec

Title: US-09-759-112a-7

Perfect score: 633

Sequence: 1 QVTLKESGPGILQPSQTLSL.....SLTAYAMDYWGQTSVTVSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	419.5	66.3	120	1 HV2B_HUMAN	P01815 homo sapien
2	407	64.3	125	1 HV2D_HUMAN	P01817 homo sapien
3	402.5	63.6	147	1 HV2B_HUMAN	P04438 homo sapien
4	395	62.4	121	1 HV2E_HUMAN	P01818 homo sapien
5	384	60.7	144	1 HV43_MOUSE	P01819 mus musculus
6	371	58.6	119	1 HV2C_HUMAN	P01816 homo sapien
7	358.5	56.6	126	1 HV2A_HUMAN	P01814 homo sapien
8	353	55.8	137	1 HV46_MOUSE	P01822 mus musculus
9	327	51.7	115	1 HV44_MOUSE	P01820 mus musculus
10	317	50.1	129	1 HV2F_HUMAN	P01824 homo sapien
11	315.5	49.8	135	1 HV2G_HUMAN	P20957 xenopus lae
12	312.5	49.4	116	1 HV60_MOUSE	P18531 mus musculus
13	309.5	48.9	146	1 HV21_HUMAN	P06331 homo sapien
14	306.5	48.4	126	1 HV3K_HUMAN	P01772 homo sapien
15	305	48.2	117	1 HV2G_HUMAN	P01825 homo sapien
16	302	47.7	121	1 HV3J_HUMAN	P01771 homo sapien
17	299.5	47.3	116	1 HV61_MOUSE	P18532 mus musculus
18	299.5	47.3	122	1 HV3G_HUMAN	P01768 homo sapien
19	299.5	47.3	136	1 HV16_MOUSE	P01783 mus musculus
20	298	47.1	113	1 HV47_MOUSE	P01823 mus musculus
21	293	46.3	111	1 HV45_MOUSE	P01821 mus musculus
22	288	45.5	117	1 HV62_MOUSE	P18533 mus musculus
23	287.5	45.4	122	1 HV3H_HUMAN	P01769 homo sapien
24	287	45.3	136	1 HV01_XENLA	P20956 xenopus lae
25	278.5	44.0	119	1 HV40_MOUSE	P01810 mus musculus
26	278	43.9	119	1 HV31_HUMAN	P01770 homo sapien
27	275.5	43.5	119	1 HV37_MOUSE	P01807 mus musculus
28	273	43.1	117	1 HV41_MOUSE	P01811 mus musculus
29	272.5	43.0	119	1 HV38_MOUSE	P01808 mus musculus
30	271.5	42.9	116	1 HV2T_HUMAN	P01781 homo sapien
31	271	42.8	117	1 HV42_MOUSE	P01812 mus musculus
32	266	42.0	119	1 HV3L_HUMAN	P01773 homo sapien
33	262.5	41.5	114	1 HV3E_HUMAN	P01763 homo sapien

34	262.5	41.5	119	1 HV3M_HUMAN	P01774 homo sapien
35	261	41.2	115	1 HV3D_HUMAN	P01765 homo sapien
36	261	41.2	115	1 HV3F_HUMAN	P01767 homo sapien
37	260.5	41.2	118	1 HV3V_HUMAN	P04419 homo sapien
38	259.5	41.0	122	1 HV20_MOUSE	P01789 mus musculus
39	256.5	40.5	119	1 HV3N_HUMAN	P01775 homo sapien
40	256	40.4	118	1 HV39_MOUSE	P01809 mus musculus
41	256	40.4	123	1 HV24_MOUSE	P01793 mus musculus
42	256	40.4	142	1 HV01_RAT	P01805 rattus norv
43	255	40.3	123	1 HV23_MOUSE	P01792 mus musculus
44	255	40.3	123	1 HV25_MOUSE	P01794 mus musculus
45	254.5	40.2	115	1 HV3S_HUMAN	P01780 homo sapien

ALIGNMENTS

RESULT 1
HV2B_HUMAN
ID HV2B_HUMAN STANDARD; PRT; 120 AA.
AC P01815;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region COR.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=70258837; PubMed=5449120;
RA Press E.M., Hogg N.M.;
RT "The amino acid sequences of the Pd fragments of two human gamma-1
RT heavy chains.";
RL Biochem. J. 117:641-660 (1970).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
CC PROTEIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR, A02089; GIHUCO.
DR HSP, P01825; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_Mc.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Glycoprotein; Pyrrolidone carboxylic acid.
FT DOMAIN 1 110
FT MOD_RES 1 1
FT DISULFD 22 94
FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .).
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13226 MW; 158A8B29AE7EEB98 CRC64;
Query Match 66.3%; Score 419.5; DB 1; Length 120;
Best Local Similarity 65.3%; Pred. No. 2.5e-36;
Matches 84; Conservative 15; Mismatches 19; Indels 5; Gaps 2;
QY 1 QVTLKESGPGILQPSQTLSLTCSFGSLSTSGMGVSWIRQPSGKGLWLAHIYWDKDKR 60
DB 1 QVTLRESGPALVKFTQLTLTCTFSGSLSTSGMVCWIRQPPGKGLWLAIRDWDDKY 60
QY 61 YNPILKRLITISKDTSSNOVFLKITSVDTSDTATYTCARRVSLTAYA--MDYWGQGSVT 118
DB 61 YNTSLETRLTISKDTSRNQVVL---TMDPVDTATYTCARITVTPAPAGYMDVWGRGTPVT 117
QY 119 VSS 121
DB 118 VSS 120

RESULT 2

HV2D_HUMAN
ID HV2D_HUMAN STANDARD; PRT; 125 AA.
AC P01817;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region MCE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RX MEDLINE=81118242; PubMed=6790622;
RA Gerber-Jenson B., Kazin A., Kenoe J.M., Scheffel C., Erickson B.W.,
Litman G.W.;
RT "Molecular basis for the temperature-dependent insolubility of
RT cryoglobulins. X. The amino acid sequence of the heavy chain variable
RL J. Immunol. 126:1212-1216(1981).
CC -1- MISCELLANEOUS: THIS CHAIN WAS DERIVED FROM A MONOCLONAL IGM
CC CRYOGLOBULIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02092; MEHUMC.
DR HSP; P01825; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR003006; Ig_LIKE.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Pyridolone carboxylic acid.
FT DOMAIN 1 113
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 125 125
SQ SEQUENCE 125 AA; 13783 MW; 7A1ADF4C40F47BB5 CRC64;

Query Match 64.3%; Score 407; DB 1; Length 125;
Best Local Similarity 63.2%; Pred. No. 5e-35;
Matches 79; Conservative 17; Mismatches 25; Indels 4; Gaps 1;
QY 1 QVTLKESGPGILQPSQTLSTLCTSGFSLSTSGVSGVSWIRQPSGKGLWLAHYWDDDKR 60
Db 1 QITLKESGPTLVKPTETLTCTFSGFSLSTSGVSGVSWIRQPSGKALEWLAFINWDDDN 60
QY 61 YNPSLKSLRTISKDTSSNQVFLKITSVDTRDTATYCA-----RVSLTAYAMYDYGQTS 116
Db 61 YSPSLRSLRTGKDTSRNQVLTITNDMPVDSGTGYCAHRPPWRFTGNLGGFDXWQGGTL 120
QY 117 VTVSS 121
Db 121 VTVSS 125

RESULT 3

HV2H_HUMAN
ID HV2H_HUMAN STANDARD; PRT; 147 AA.
AC P04438;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-II region SSS precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

SEQUENCE FROM N.A.
RX MEDLINE=84298107; PubMed=6089186;
RA Takahashi N., Noma T., Honjo T.;
RT "Rearranged immunoglobulin heavy chain variable region (VH)
RT pseudogene that deletes the second complementarity-determining
RT region.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5194-5198(1984).
DR PIR; A02090; G2HUCS.
DR HSP; P01825; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig_LIKE.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 147 IG HEAVY CHAIN V-II REGION SSS.
FT DOMAIN 20 118 V SEGMENT.
FT DOMAIN 119 132 D SEGMENT.
FT DOMAIN 133 147 J SEGMENT.
FT NON_TER 147 147
SQ SEQUENCE 147 AA; 16323 MW; FCBDB3D00FB6666 CRC64;
Query Match 63.6%; Score 402.5; DB 1; Length 147;
Best Local Similarity 62.3%; Pred. No. 1.8e-34;
Matches 76; Conservative 16; Mismatches 23; Indels 7; Gaps 1;
QY 1 QVTLKESGPGILQPSQTLSTLCTSGFSLSTSGVSGVSWIRQPSGKGLWLAHYWDDDKR 60
Db 20 QVNLRSGPALVKATHITLTCTFSGVSVNTRGMSVSWIRQPSGKALEWLAIDWDDDKY 79
QY 61 YNPSLKSLRTISKDTSSNQVFLKITSVDTRDTATYCA-----RVSLTAYAMYDYGQ 113
Db 80 YGTSLETRLTISKDTSKNQVVLKYNMNDPADTATYTCARMQVTWREVMITSNAFDIWGQ 139
QY 114 GT 115
Db 140 GT 141
RESULT 4
HV2E_HUMAN
ID HV2E_HUMAN STANDARD; PRT; 121 AA.
AC P01818;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region HE.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RX MEDLINE=70114712; PubMed=5264153;
RA Cunningham B.A., Pflumm M.N., Rutishauser U., Edelman G.M.;
RT "Subgroups of amino acid sequences in the variable regions of
RT immunoglobulin heavy chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 64:997-1003(1969).
CC -1- MISCELLANEOUS: THIS GAMMA-1 CHAIN WAS ISOLATED FROM A MYELOMA
CC PROTEIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02093; GIUHE.
DR HSP; P01825; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig_LIKE.
DR InterPro; IPR003006; Ig_MHC.

```
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT DOMAIN 1 120
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13483 MW; 88A5082C273753B4 CRC64;

Query Match 62.4%; Score 395; DB 1; Length 121;
Best Local Similarity 61.5%; Pred. No. 8.3e-34;
Matches 75; Conservative 20; Mismatches 25; Indels 2; Gaps 2;

QY 1 QVTLKESGPGIQLPSQTLISLTCFSFSLSTSGMGVSWIRQPSGKGLWLAH-IYWDK 59
DB 1 QVTLKENGPTLVKPTETLTCTLSGLSTTDGAVGWIRQPGRALEWLAHLLYWDK 60

QY 60 RYNSPLKSLRTISKDTSSNOVFLKITSVDTRDTATYTCARRVSLTAYAMYWGQTSVTV 119
DB 61 RYNSPLKSLRTISKDTSSNOVFLKITSVDTRDTATYTCARRVSLTAYAMYWGQTSVTV 119

QY 120 SS 121
DB 120 SS 121

RESULT 5
HV43_MOUSE
ID HV43_MOUSE STANDARD; PRT; 144 AA.
AC P01819;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MOPC 141 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81012133; PubMed=6774259;
RA Sakano H., Maki R., Kuroawa Y., Roeder W., Tonegawa S.;
RT "Two types of somatic recombination are necessary for the generation
of complete immunoglobulin heavy-chain genes.";
RL Nature 286:676-683(1980).
CC -!- MISCELLANEOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A
DIFFERENTIATED GENE ISOLATED FROM A MYELOMA THAT SECRETES IGG2B.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC -----
CC EMBL; V00768; CAA24149.1; --
DR PIR; A02094; G2MS14.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 144 IG HEAVY CHAIN V REGION MOPC 141.
FT DOMAIN 20 130 IG-LIKE.
FT NON_TER 144 144
SQ SEQUENCE 144 AA; 15759 MW; 8E47A7CB3706D30A CRC64;
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Query Match 60.7%; Score 384; DB 1; Length 144;
Best Local Similarity 60.9%; Pred. No. 1.4e-32;
Matches 78; Conservative 17; Mismatches 23; Indels 10; Gaps 3;

QY 1 QVTLKESGPGIQLPSQTLISLTCFSFSLSTSGMGVSWIRQPSGKGLWLAHLYWDK 60
DB 20 QVTLKESGPGIQLPSQTLISLTCFSFSLSTSGMGVSWIRQPSGKGLWLAHLYWDK 60
QY 61 YNPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYTCARRVSLTAY-----AMDYWGQ 113
DB 78 YNPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYTCARRVSLTAY-----AMDYWGQ 113

QY 114 GTSVTSS 121
DB 137 GTSVTSS 144
```

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RESULT 6
HV2C_HUMAN
ID HV2C_HUMAN STANDARD; PRT; 119 AA.
AC P01816;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region DAW.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=70258837; PubMed=5449120;
RA Press E.M., Hogg N.M.;
RT "The amino acid sequences of the Fd fragments of two human gamma-1
heavy chains.";
RL Biochem. J. 117:641-660(1970).
CC -!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGG1 ISOLATED FROM THE
SERUM OF A PATIENT WITH HYPERGAMMAGLOBULINEMIA.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02091; G1HUDW.
DR HSSP; P01789; 1MCP.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT DOMAIN 1 113
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13045 MW; 4E13E00214BAD789 CRC64;
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Query Match 58.6%; Score 371; DB 1; Length 119;
Best Local Similarity 61.3%; Pred. No. 2.4e-31;
Matches 76; Conservative 15; Mismatches 25; Indels 8; Gaps 3;

QY 1 QVTLKESGPGIQLPSQTLISLTCFSFSLSTSGMGVSWIRQPSGKGLWLAHLYWD---D 57
DB 1 QVTLKESGPGIQLPSQTLISLTCFSFSLSTSGMGVSWIRQPSGKGLWLAHLYWD---D 57
QY 58 DKRYNSPLKSLRTISKDTSSNOVFLKITSVDTRDTATYTCARRVSLTAYAMYWGQTSV 117
DB 58 DKRYNSPLKSLRTISKDTSSNOVFLKITSVDTRDTATYTCARRVSLTAYAMYWGQTSV 117

QY 118 TVSS 121
DB 116 TVSS 119
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RESULT 7
HV2A_HUMAN STANDARD; PRT; 126 AA.
AC P01814;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region OU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=74005511; PubMed=4742735;
RA Putnam F.W., Florent G., Paul C., Shinoda T., Shimizu A.;
RT "Complete amino acid sequence of the Mu heavy chain of a human IgM
immunoglobulin."
RL Science 182:287-291(1973).
CC -I- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S
MACROGLOBULIN.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02088; MHUOU.
DR HSSP; P01825; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT DOMAIN 1 113
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 97
FT NON_TER 126 126
FT SEQUENCE 126 AA; 14276 MW; A85C0BB0DABC296F CRC64;
SQ
Query Match 56.6%; Score 358.5; DB 1; Length 126;
Best Local Similarity 60.3%; Pred. No. 4.9e-30;
Matches 76; Conservative 19; Mismatches 26; Indels 5; Gaps 2;
QY 1 QVTLKSGPILQPSQTLSTLSTGSGFSLSTGSGVSWIRQPSGKLEWLAHYWDDKR 60
Db ||||| :||: ||||| ||||| ||||| ||||| ||||| :||:
QY 1 QVTLTSGPALVKPQPLTLTCTFSGFSLSTSRMYSWIRRPFGKALEWLAIBBDKPY 60
Db ||||| :||: ||||| ||||| ||||| ||||| ||||| :||:
QY 61 YNPSLRLTISKDTSSNQVFLKITSVDTRDTATYCARRV-SLTA---YAMDYWGQT 115
Db :||: ||||| :||: ||||| ||||| ||||| ||||| ||||| :||:
QY 61 WTSLSRLTSLSKNDKSNQVLLIMINVPVDTATYCARVNSVMAGYVYVYDVGKGT 120
Db :||: ||||| :||: ||||| ||||| ||||| ||||| ||||| :||:
QY 116 SVTVSS 121
Db 121 TVTVSS 126
RESULT 8
HV46_MOUSE STANDARD; PRT; 137 AA.
AC P01822;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig heavy chain V region MOPC 315 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89239351; PubMed=2497341;
```

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RA Rinfret A., Horne C., Dorrington K.J., Klein M.;
RT "Cloning, sequencing and expression of the rearranged MOPC 315 VH
gene segment.";
RL Mol. Immunol. 26:431-434 (1989).
RN [2]
RP SEQUENCE OF 1-31.
RX MEDLINE=78094475; PubMed=414225;
RA Jilka R.L., Pestka S.;
RT "Amino acid sequence of the precursor region of MOPC-315 mouse
immunoglobulin heavy chain.";
RL Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696(1977).
RN [3]
RP SEQUENCE OF 1-21.
RX MEDLINE=79148758; PubMed=428562;
RA Schechter I., Wolf O., Zemell R., Burstein Y.;
RT "Structure and function of immunoglobulin genes and precursors.";
RL Fed. Proc. 38:1839-1845(1979).
RN [4]
RP SEQUENCE OF 19-136.
RX MEDLINE=74170779; PubMed=4524622;
RA Francis S.H., Leslie R.G.Q., Hood L., Eisen H.N.;
RT "Amino-acid sequence of the variable region of the heavy (alpha)
chain of a mouse myeloma protein with anti-hapten activity.";
RL Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127(1974).
RN [5]
RP REVISION TO 53.
RX MEDLINE=77244979; PubMed=268248;
RA Hood L., Margolies M.N., Givol D., Zakut R.;
RL Unpublished results, cited by:
RA Padlan E.A., Davies D.R., Pecht I., Givol D., Wright C.;
RL Cold Spring Harb. Symp. Quant. Biol. 41:627-637(1977).
CC -I- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA
PROTEIN THAT HAS ANTI-DINITROPHENYL ACTIVITY.
CC
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CC -----
CC EMBL; M27638; AAA61337.1; -.
DR EMBL; X07880; CAA30727.1; -.
DR PIR; P01022; AVMS35.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 18
FT CHAIN 19 137
FT DOMAIN 19 48
FT DOMAIN 49 54
FT DOMAIN 55 68
FT DOMAIN 69 84
FT DOMAIN 85 116
FT DOMAIN 117 126
FT DOMAIN 127 137
FT DISULFID 40 114
FT CONFLICT 15 15
FT CONFLICT 15 15
FT CONFLICT 77 78
FT CONFLICT 102 102
FT CONFLICT 123 123
FT NON_TER 137 137
SQ SEQUENCE 137 AA; 15399 MW; FB3828304C2B81DC CRC64;
Query Match 55.8%; Score 353; DB 1; Length 137;
Best Local Similarity 59.2%; Pred. No. 2e-29;
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Matches 71; Conservative 19; Mismatches 28; Indels 2; Gaps 2;
 QY 2 VTLKESGPGILOPQSOTLSLTCFSFGSLSTSGMGVSWIRQPSGKGLWLAHIYWDGDDKEY 61
 Db 20 VQLQESGPGILVKSQSLSLTCTSVGTGSI-TSGYFWNIQPPGKGLWLGKIDGSGNY 78
 QY 62 NPSLKSLRTISKDTSSNQVFLKITSVDTTRDTATYYCARRVSLTAYAMYWGQTSVTSS 121
 Db 79 NPSLKSRVSTRTDSENQVFLKITSVDTTRDTATYYCAGD-NDHLYYFYWGQGTTLTVSS 137
 RESULT 9
 HV44_MOUSE
 ID HV44_MOUSE STANDARD; PRT; 115 AA.
 AC P01820;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region P014 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81012133; PubMed=6774258;
 RA Sakano H., Maki R., Kuroiwa Y., Roeder W., Tonegawa S.;
 RT "Two types of somatic recombination are necessary for the generation
 of complete immunoglobulin heavy-chain genes.";
 RL Nature 286:676-683(1980).
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC
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 CC
 CC ENBL; V00767; CAA24148.1; -
 DR PIR; A02095; HVMS14.
 DR PDB; 1A7N; 29-APR-98.
 DR PDB; 1A7O; 29-APR-98.
 DR PDB; 1A7P; 29-APR-98.
 DR PDB; 1A7R; 29-APR-98.
 DR PDB; 1G7H; 17-JAN-01.
 DR PDB; 1G7I; 17-JAN-01.
 DR PDB; 1G7J; 17-JAN-01.
 DR PDB; 1G7M; 17-JAN-01.
 DR PDB; 43C9; 24-JUL-02.
 DR PDB; 43CA; 24-JUL-02.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Signal; 3D-structure.
 FT SIGNAL 1
 FT CHAIN 19
 FT DOMAIN 20
 FT NON TER 115
 FT DOMAIN 20
 FT NON TER 115
 SQ SEQUENCE 115 AA; 12447 MW; 7569DDA4A4843D500 CRC64;
 Query Match 51.7%; Score 327; DB 1; Length 115;
 Best Local Similarity 54.3%; Pred. No. 7.6e-27;
 Matches 63; Conservative 14; Mismatches 19; Indels 2; Gaps 1;
 QY 1 QVTLKESGPGILOPQSOTLSLTCFSFGSLSTSGMGVSWIRQPSGKGLWLAHIYWDGDDKEY 60
 Db 20 QVQLKESGPGILVAPQSLSITCTVSGFSL--TGYNWVWVQPPGKGLWLGWIDGSDTD 77

QY 61 YNPSLKSLRTISKDTSSNQVFLKITSVDTTRDTATYYCA 98
 Db 78 YNSALKSRLSLSKNSKNSQVFLKNSLQTDTRDTATYYCA 115
 RESULT 10
 HV2F_HUMAN
 ID HV2F_HUMAN STANDARD; PRT; 129 AA.
 AC P01824;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-II region WAH.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=8222235; PubMed=6806818;
 RA Takahashi N., Tetaert D., Debuire B., Lin L.-C., Putnam F.W.;
 RT "Complete amino acid sequence of the delta heavy chain of human
 immunoglobulin D.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGD MYELOMA
 PROTEIN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A02099; D2HWA.
 DR HSSP; P01825; 7FAB.
 DR GlycoSuiteDB; P01824; -
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006985; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1
 FT NON TER 129
 FT DOMAIN 113
 IG-LIKE.
 SQ SEQUENCE 129 AA; 14117 MW; D5D53D47ABE51319 CRC64;
 Query Match 50.18; Score 317; DB 1; Length 129;
 Best Local Similarity 49.6%; Pred. No. 9.2e-26;
 Matches 64; Conservative 18; Mismatches 39; Indels 8; Gaps 1;
 QY 1 QVTLKESGPGILOPQSOTLSLTCFSFGSLSTSGMGVSWIRQPSGKGLWLAHIYWDGDDKEY 60
 Db 1 RLQQLKESGPGILVAPQSLSITCTVSGGPIRTTGYWGWIRQPPGKGLWIGGVYTGSIY 60
 QY 61 YNPSLKSLRTISKDTSSNQVFLKITSVDTTRDTATYYCARRVSLTAY-----ANDYWG 112
 Db 61 YNPSLRGRVTISVDTSRNQVFLKITSVDTTRDTATYYCARRVSLTAY-----ANDYWG 120
 QY 113 QGTSVTSS 121
 Db 121 QGTTVHSS 129
 RESULT 11
 HV02_XENLA
 ID HV02_XENLA STANDARD; PRT; 135 AA.
 AC P20957;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region XIG14 precursor (Fragment).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.

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OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88176921; PubMed=2451244;
RA Schwager J., Mikoryak C.A., Steiner L.A.;
RT "Amino acid sequence of heavy chain from Xenopus laevis IgM deduced
RT from cDNA sequence: implications for evolution of immunoglobulin
RT domains.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249 (1988).
CC -1- SIMILARITY. Contains 1 immunoglobulin-like domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: J03632; AAA49791.1; -
CC PIR: B31933; B31933.
CC HSP: P01810; 2FBU.
CC InterPro: IPR007110; Ig-like.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003596; Ig_v.
CC Pfam: PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT NON_TER 1 1
FT SIGNAL <1 18
FT CHAIN 19 135 IG HEAVY CHAIN V REGION XIG14.
FT DOMAIN 20 138 IG-LIKE.
FT NON_TER 135 135
SQ SEQUENCE 135 AA; 15080 MW; EBC467105C00732E CRC64;

Query Match 49.8%; Score 315.5; DB 1; Length 135;
Best Local Similarity 52.1%; Pred. No. 1.4e-25;
Matches 62; Conservative 20; Mismatches 34; Indels 3; Gaps 2;

QY 3 TLKESGPGILQPSQTLSTCSFSGSLSTSGMGVSWIROPKGLWLAHIYWDCKRYN 62
DB 20 TLQESGPGILQPSQTLSTCSFSGSLSTSGMGVSWIROPKGLWLAHIYWDCKRYN 77
QY 63 PSLSKRLTISKDTSSNOVFLKITSVDTRTATYTCARRVSLTAYAVDYGQTSVTVSS 121
DB 78 DSLKRNRTIKNGKKQVILQNGMEVKDTAMYTCAREYA-SGYNFDWGGQTMVTVTS 135

RESULT 12
HV60 MOUSE STANDARD; PRT; 116 AA.
AC P18531;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region M315 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/CJ;
RA Levine N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019 (1989).
DR PIR; J05059; HVMS31.
DR HSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
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DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 18
FT CHAIN 19 116 IG HEAVY CHAIN V REGION M315.
FT DOMAIN 19 48 FRAMEWORK-1.
FT DOMAIN 49 53 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 54 67 FRAMEWORK-2.
FT DOMAIN 68 84 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 85 116 FRAMEWORK-3.
FT DISULFID 40 114 BY SIMILARITY.
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 13095 MW; 4562E03E53DC9E10 CRC64;

Query Match 49.4%; Score 312.5; DB 1; Length 116;
Best Local Similarity 60.2%; Pred. No. 2.4e-25;
Matches 59; Conservative 18; Mismatches 20; Indels 1; Gaps 1;

QY 2 VTLESGPGILQPSQTLSTCSFSGSLSTSGMGVSWIROPKGLWLAHIYWDCKRY 61
DB 20 VQLQESGPGILQPSQTLSTCSFSGSLSTSGMGVSWIROPKGLWLAHIYWDCKRY 78
QY 62 NPSLSKRLTISKDTSSNOVFLKITSVDTRTATYTCAR 99
DB 79 NPSLSKRLTISKDTSSNOVFLKITSVDTRTATYTCAR 116

RESULT 13
HV21 HUMAN STANDARD; PRT; 146 AA.
AC P06331;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-II region ARH-77 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85205332; PubMed=3922855;
RA Kudo A., Ishihara T., Nishimura Y., Watanabe T.;
RT "A cloned human immunoglobulin heavy chain gene with a novel direct-
RT repeat sequence in 5' flanking region.";
RL Gene 33:181-189 (1985).
DR PIR; A02101; GIH02.
DR HSP; P01825; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 146 IG HEAVY CHAIN V-II REGION ARH-77.
FT DOMAIN 20 117 V SEGMENT.
FT DOMAIN 118 127 D SEGMENT.
FT DOMAIN 128 146 J SEGMENT.
FT DISULFID 42 115 BY SIMILARITY.
FT NON_TER 146 146
SQ SEQUENCE 146 AA; 16228 MW; 8D7FD52BB218171F CRC64;

Query Match 48.9%; Score 309.5; DB 1; Length 146;
Best Local Similarity 52.3%; Pred. No. 6.3e-25;
Matches 67; Conservative 14; Mismatches 38; Indels 9; Gaps 2;
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QY 1 QVTLKESGPIQLPSQTLSTCSFSGFSLSTGSGVSWIQPSKGLWLAHIYWDK 60
 Db 21 QVQLQWAGLVKPSSETLSLTCAVFGSP--SGVYMSWIRQPPGRGLEWIGNHSGSTN 78
 QY 61 YNPSLKSLRTISKDTSSNQVFLKITSVDTRDTATYTCAREVSLTA-----YADYWGQ 113
 Db 79 YKTSLSKSRVTSISLDTSKVLSLSSVTAADTAVYTCARGLLGWNVDDYVYGVNDVWGQ 138
 QY 114 GTSVTYVSS 121
 Db 139 GTTVTVSS 146

RESULT 14
 HV3K_HUMAN STANDARD; PRT; 126 AA.
 AC P01772;
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE IG heavy chain V-II region KOL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE AND DISULFIDE BONDS.
 RX MEDLINE=83289131; PubMed=684994;
 RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
 RT "Three-dimensional structure determination of antibodies. Primary
 structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=81072295; PubMed=7441755;
 RA Marquart M., Deisenhofer J., Huber R., Palm W.;
 RT "Crystallographic refinement and atomic models of the intact
 immunoglobulin molecule Kol and its antigen-binding fragment at 3.0 A
 and 1.0-A resolution.";
 RL J. Mol. Biol. 141:369-391(1980).
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A02055; GIHKUL.
 DR PDB; 2FB4; 12-JUL-89.
 DR PDB; 2IG2; 12-JUL-89.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 KW Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic acid.
 FT DOMAIN 1 112
 FT MOD_RES 1 1
 FT DISULFID 22 96
 FT DISULFID 105 110
 FT STRAND 3 7
 FT STRAND 11 12
 FT TURN 14 15
 FT STRAND 18 25
 FT STRAND 29 31
 FT STRAND 34 39
 FT TURN 41 42
 FT STRAND 45 51
 FT TURN 53 54
 FT STRAND 58 60
 FT STRAND 62 64
 FT HELIX 65 65
 FT TURN 66 67
 FT STRAND 68 73
 FT TURN 74 77

FT STRAND 78 83
 FT HELIX 88 90
 FT STRAND 92 99
 FT STRAND 106 106
 FT TURN 107 108
 FT STRAND 109 109
 FT STRAND 113 116
 FT STRAND 120 124
 FT NON TER 126 126
 SQ SEQUENCE 126 AA; 13718 MW; E4D71B52B16F8776 CRC64;

Query Match 48.4%; Score 306.5; DB 1; Length 126;
 Best Local Similarity 50.4%; Pred. No. 1.1e-24;
 Matches 65; Conservative 18; Mismatches 35; Indels 11; Gaps 4;

QY 1 QVTLKESGPIQLPSQTLSTCSFSGFSLSTGSGVSWIQPSKGLWLAHIYWDK--D 58
 Db 1 QVQLVESGGGVQPGSRSLRLSCSSGSIFFSYAM--YVTRQAPGKGLWVA--IWDGSD 57
 QY 59 KYNPFLKSLRTISKDTSSNQVFLKITSVDTRDTATYTCARR-----VSLTAYADYWG 112
 Db 58 QYADSVKGRFTISRDNKNTFLQMDSLRPDTGVYFCARDGGHGFCSASCFGPDYWG 117
 QY 113 QGTSVTYVSS 121
 Db 118 QGTPVTYVSS 126

RESULT 15
 HV2G_HUMAN STANDARD; PRT; 117 AA.
 AC P01825;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE IG heavy chain V-II region NEMM.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=77242302; PubMed=407927;
 RA Poljak R.J., Nakashima Y., Chen B.L., Konigsberg W.;
 RT "Amino acid sequence of the VH region of a human myeloma
 immunoglobulin (IgG New).";
 RL Biochemistry 16:3412-3420(1977).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FAB FRAGMENT.
 RX MEDLINE=78066916; PubMed=618887;
 RA Saul F.A., Amzel L.M., Poljak R.J.;
 RT "Preliminary refinement and structural analysis of the Fab fragment
 from human immunoglobulin new at 2.0-A resolution.";
 RL J. Biol. Chem. 253:585-597(1978).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
 PROTEIN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A90404; GIHUNM.
 DR PDB; 7FAB; 31-JAN-94.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 KW Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic acid.
 FT DOMAIN 1 111
 FT MOD_RES 1 1
 FT STRAND 3 7
 FT STRAND 11 12


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FT TURN 14 15
FT STRAND 18 25
FT TURN 30 31
FT STRAND 33 39
FT TURN 41 42
FT STRAND 46 51
FT TURN 53 54
FT STRAND 57 59
FT HELIX 61 63
FT TURN 64 66
FT STRAND 67 72
FT TURN 73 76
FT STRAND 77 82
FT HELIX 87 89
FT STRAND 91 98
FT STRAND 104 107
FT STRAND 111 115
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12790 MW; 2DA47B509562D237 CRC64;

Query Match 48.2%; Score 305; DB 1; Length 117;
Best Local Similarity 49.6%; Pred. No. 1.4e-24;
Matches 60; Conservative 24; Mismatches 33; Indels 4; Gaps 2;

QY 1 QVTLKESGFGILQPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSKGLEWLAIHYWDDDKR 60
Db ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::
1 QVQLEQSGFGLVRPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSKGLEWLAIHYWDDDKR 58
QY 61 YNPPLKSLRTISKDTSSNOVELKITSDTRDTATYCCARRVSLTAYAMDYWGQGTSTVTS 120
Db 59 DTTPLRSRVTMLVDTSKNQPSLRLSSVTADTAVYICAR--NLIAGCIDVWGQGTSTVTS 116
QY 121 S 121
Db 117 S 117
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Search completed: January 14, 2004, 19:11:51
Job time : 12 secs


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Db 1 QVTLKESGPGILQPSQTLSTCTCFSGFSLTSCMDVGWIRQPPGKALEWLAHYWDDDKR 60
QY 61 YNPGLKSLRTISKDTSSNQVFLKITSVDTRDTATYCARVSLTAYAMDYWGQGSVTVS 120
Db 61 YNPGLKSLRTISKDTSSNQVFLKITSVDTRDTATYCARVSLTAYAMDYWGQGSVTVS 120
QY 121 S 121
Db 121 S 121

RESULT 2
Q99NG4 PRELIMINARY; PRT; 121 AA.
AC Q99NG4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Single chain Fv (Fragment).
OS Mus musculus (Mouse).
CG Plasmid pHEN1.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/C;
RX MEDLINE=98169018; PubMed=9510199;
RA Hawlicsek H., Frank R., Hennecke M., Baensch M., Sohns B., Arseniev L.,
BAutsch W., Koja A., Klos A., Koehl J.,
RT "Site-Directed C3a-Receptor Antibodies from Phage Display Libraries.";
RL J. Immunol. 160:2947-2958(1998).
DR EMBL; AJ222590; CAA10890.1; -.
DR HSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Plasmid.
FT NON TER 1 121
FT NON TER 121 121
SQ SEQUENCE 121 AA; 13255 MW; D293E4EBC8C59D5B CRC64;

Query Match 63.0%; Score 398.5; DB 11; Length 121;
Best Local Similarity 64.8%; Pred. No. 4.1e-36;
Matches 79; Conservative 17; Mismatches 23; Indels 3; Gaps 2;

QY 1 QVTLKESGPGILQPSQTLSTCTCFSGFSLTSCMDVGWIRQPPGKALEWLAHYWDDDKR 60
Db 1 QVQLKESGPGILVAPSQSLSTCTVSGFPLTSH--GVSWVRQPPGKGLWLGIVGDNKTK 58
QY 61 YNPGLKSLRTISKDTSSNQVFLKITSVDTRDTATYCARVSLTAYAMDYWGQGSVTV 119
Db 59 YHSAISRLSISKDNKSQVFLKNSLQTDATYCARHYKYANYAMDYWGQGSVTV 118
QY 120 SS 121
Db 119 SS 120

RESULT 3
Q91X92 PRELIMINARY; PRT; 482 AA.
AC Q91X92;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Unknown (Protein for MGC:18822).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

```
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011181; AAH11181.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
SQ SEQUENCE 482 AA; 51865 MW; 312E01F9C1BC7F3C CRC64;

Query Match 58.5%; Score 370.5; DB 11; Length 482;
Best Local Similarity 61.2%; Pred. No. 3e-32;
Matches 74; Conservative 17; Mismatches 27; Indels 3; Gaps 2;

QY 1 QVTLKESGPGILQPSQTLSTCTCFSGFSLTSCMDVGWIRQPPGKALEWLAHYWDDDKR 60
Db 20 QVQLKESGPGILVAPSQSLSTCTVSGFPLTSH--YAIISWRQPPGKGLWLGIVTGGVTN 77
QY 61 YNPGLKSLRTISKDTSSNQVFLKITSVDTRDTATYCARVSLTAYAMDYWGQGSVTVS 120
Db 78 YNSALKSLRSISKDNKSQVFLKNSLQTDATYCARVSLTAYAMDYWGQGSVTVS 136
QY 121 S 121
Db 137 S 137

RESULT 4
Q96KX8 PRELIMINARY; PRT; 496 AA.
AC Q96KX8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016369; AAH16369.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 496 AA; 53391 MW; D346929849040D69 CRC64;

Query Match 57.1%; Score 361.5; DB 4; Length 496;
Best Local Similarity 59.2%; Pred. No. 3.1e-31;
Matches 74; Conservative 17; Mismatches 29; Indels 5; Gaps 2;

QY 1 QVTLKESGPGILQPSQTLSTCTCFSGFSLTSCMDVGWIRQPPGKALEWLAHYWDDDKR 60
Db 20 QVQLKESGPGILVAPSQSLSTCTVSGFPLTSH--YAIISWRQPPGKGLWLGIVTGGVTN 79
QY 61 YNPGLKSLRTISKDTSSNQVFLKITSVDTRDTATYCARVSLTAYAMDYWGQGSVTVS 116
Db 80 YNPGLKSLRTISKDTSSNQVFLKITSVDTRDTATYCARVSLTAYAMDYWGQGSVTVS 138
```

QY 117 VTSS 121
DB 139 VTSS 143

RESULT 5

Q9UL73 PRELIMINARY; PRT; 119 AA.
AC Q9UL73; 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035041; AAD56277.1; -.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1 1
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13219 MW; 1BD86B6420EA0BE CRC64;

Query Match 57.0%; Score 361; DB 4; Length 119;
Best Local Similarity 57.7%; Pred. No. 5.5e-32;
Matches 71; Conservative 16; Mismatches 32; Indels 2; Gaps 1;
QY 1 QVTLKESGPGILQPSQTLTSLTCSFGSFLSTSGMGVSWIRQPSGKLEWLAHIYWDKRR 60
DB 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISCIYYW--SWIRQPPGKLEWIGIYVSGSTN 58
QY 61 YNPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQTSVTVS 120
DB 59 YFSLKSRVTISVDKSNQFSLKLTSLTAADTAVYFCARLSNKGPFYFDYWGQGLTVTVS 118
QY 121 S 121
DB 119 S 119

RESULT 6

O43234 PRELIMINARY; PRT; 97 AA.
AC O43234;
DT 01-JUN-1998 (T-EMBLrel. 06, Created)
DT 01-JUN-1998 (T-EMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Rheumatoid factor RF-ET13 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Borretzen M., Natvig J.B., Thompson K.M.;
RT "Heterogenous Rf structures between and within healthy individuals are not related to HLA DRE1*0401."
RL Mol. Immunol. 0:0-0(1997).

DR EMBL; AF035802; AAB8534.1; -.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1 1
FT NON_TER 97 97
SQ SEQUENCE 97 AA; 10748 MW; DDC0BF47B9AA812D CRC64;
Query Match 56.2%; Score 356; DB 4; Length 97;
Best Local Similarity 58.0%; Pred. No. 1.5e-31;
Matches 66; Conservative 16; Mismatches 15; Indels 0; Gaps 0;
QY 3 TLKESGPGILQPSQTLTSLTCSFGSFLSTSGMGVSWIRQPSGKLEWLAHIYWDKRRYN 62
DB 1 TLKESGPGALVKPTETLTCTVSGFSLNRMGVSWIRQPPGKAVEWLAHIFANDEKSYS 60
QY 63 PSLKSRLTISKDTSSNOVFLKITSVDTRDTATYYCAR 99
DB 61 TSLKSRLTISKDTSKSQVLTMTNMDPMDTATYYCAR 97

RESULT 7

Q96EY0 PRELIMINARY; PRT; 613 AA.
AC Q96EY0;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011857; AAH1857.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;

Query Match 56.0%; Score 354.5; DB 4; Length 613;
Best Local Similarity 59.0%; Pred. No. 2.4e-30;
Matches 72; Conservative 16; Mismatches 31; Indels 3; Gaps 2;
QY 1 QVTLKESGPGILQPSQTLTSLTCSFGSFLSTSGMGVSWIRQPSGKLEWLAHIYWDKRR 60
DB 20 QVQLQESGPGLVKPSSETLSLTCTVSGSISCIYYW--SWIRQPPGKLEWIGIYVSGSTN 77
QY 61 YNPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYYCARRV--SLTAYAMDYWGQTSVTV 119
DB 78 YNPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYYCARRV--SLTAYAMDYWGQTSVTV 137
QY 120 SS 121
DB 138 SS 139
RESULT 8
Q99M22 PRELIMINARY; PRT; 479 AA.
ID Q99M22

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AC Q9W22;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 52.0 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002091; AAH02091.1; -.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 479 AA; 51992 MW; 768839A138918892 CRC64;

Query Match 54.2%; Score 343; DB 11; Length 479;
Best Local Similarity 57.0%; Pred. No. 3.2e-29;
Matches 69; Conservative 20; Mismatches 26; Indels 6; Gaps 3;

QY 2 VTLKSGPGIQLPQSOTLSLTCSPGFSLSSTGSGVSWIRQPSGKGLWLAHIYDDDKR 61
Db 20 VQLQSGPGLVPSGLSLTSCVTGYSI-TSGYYWNIWIRQPSGKGLWLVINDGSNNY 78

QY 62 NPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTA-YMDYWGQGVTS 120
Db 79 NPSLKNRISITRDTSKNQVFLKINSVTTEDTATYTCASR---GYSWFPNNGQGLTVTS 134

QY 121 S 121
Db 135 A 135

RESULT 9
Q8WUX4 PRELIMINARY; PRT; 588 AA.
AC Q8WUX4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019235; AAH19235.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 5.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 588 AA; 64438 MW; FC60DBAD82B39FD7 CRC64;

Query Match 53.9%; Score 341; DB 4; Length 588;
Best Local Similarity 55.9%; Pred. No. 6.9e-29;
Matches 71; Conservative 15; Mismatches 33; Indels 8; Gaps 2;
```

```
QY 1 QVTLKSGPGIQLPQSOTLSLTCSPGFSLSSTGSGVSWIRQPSGKGLWLAHIYDDDKR 60
Db 20 QVQLQWAGAGLLKPSSETLSLTCTGVGGSF--SGYYWNIWIRQPSGKGLWIGINHSNSTN 77

QY 61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTA-----YMDYWGQ 114
Db 78 YNPSLKSRLTISVDTSKKQLSLSSVNAADTAVYTCARVITRASPTDGRYGMVDWGQ 137

QY 115 TSVTVSS 121
Db 138 TTVTVSS 144

RESULT 10
Q9BU10 PRELIMINARY; PRT; 597 AA.
AC Q9BU10;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002963; AAH02963.1; -.
DR HSP; P01825; 7FAB.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 5.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;

Query Match 53.9%; Score 341; DB 4; Length 597;
Best Local Similarity 55.9%; Pred. No. 7e-29;
Matches 71; Conservative 15; Mismatches 33; Indels 8; Gaps 2;

QY 1 QVTLKSGPGIQLPQSOTLSLTCSPGFSLSSTGSGVSWIRQPSGKGLWLAHIYDDDKR 60
Db 20 QVQLQWAGAGLLKPSSETLSLTCTGVGGSF--SGYYWNIWIRQPSGKGLWIGINHSNSTN 77

QY 61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTA-----YMDYWGQ 114
Db 78 YNPSLKSRLTISVDTSKKQLSLSSVNAADTAVYTCARVITRASPTDGRYGMVDWGQ 137

QY 115 TSVTVSS 121
Db 138 TTVTVSS 144

RESULT 11
Q96AA6 PRELIMINARY; PRT; 618 AA.
AC Q96AA6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
```

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RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017356; AAH17356.1;
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 618 AA; 67758 MW; 96DBD4C7C696E0A6 CRC64;

Query Match 53.9%; Score 341; DB 4; Length 618;
Best Local Similarity 55.9%; Pred. No. 7.4e-29;
Matches 71; Conservative 15; Mismatches 33; Indels 8; Gaps 2;

QY 1 QVTLKESGPGILOPSTLSITCSFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 60
Db 20 QVQLQWQAGLLKPSLTSLTCTGVYGGSF--SGYVWSWIRQPPGKLEWIGINHSGETN 77
QY 61 YNPSLKSRITISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTA-----YAMDYWGQG 114
Db 78 YNPSLKSRVITISVDTSKQLSLKSSVNAADTAVYTCARVITRASPCTDGRYGMVWGQG 137
QY 115 TSVTVSS 121
Db 138 TTVTVSS 144

RESULT 12
Q9BQ88 PRELIMINARY; PRT; 597 AA.
AC Q9BQ88;
DT 01-JUN-2001 (TrEMBLrel. 17, Created).
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006180; AAH06180.1;
DR EMBL; BC001872; AAH01872.1;
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;

Query Match 53.4%; Score 338; DB 4; Length 597;
Best Local Similarity 55.9%; Pred. No. 1.5e-28;
Matches 71; Conservative 15; Mismatches 33; Indels 8; Gaps 2;

QY 1 QVTLKESGPGILOPSTLSITCSFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 60
Db 20 QVQLQWQAGLLKPSLTSLTCTGVYGGSF--SGYVWSWIRQPPGKLEWIGINHSGETN 77
QY 61 YNPSLKSRITISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTA-----YAMDYWGQG 114
Db 78 YNPSLKSRVITISVDTSKQLSLKSSVNAADTAVYTCARVITRASPCTDGRYGMVWGQG 137
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QY 115 TSVTVSS 121
Db 138 TTVTVSS 144

RESULT 13
Q95973 PRELIMINARY; PRT; 150 AA.
AC Q95973;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-2003 (TrEMBLrel. 23, Last annotation update)
DE VHA heavy chain variable region precursor (Fragment).
GN IGM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
RL "Clonal proliferation of Igm secreting B cell in the synovium of Behcet's patient with arthritis.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF103795; AAC79084.1;
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 >150 VHA HEAVY CHAIN VARIABLE REGION.
FT NON TER 150
SQ SEQUENCE 150 AA; 16315 MW; 85664E04938AA7C9 CRC64;

Query Match 53.3%; Score 337.5; DB 4; Length 150;
Best Local Similarity 55.4%; Pred. No. 2.9e-29;
Matches 67; Conservative 19; Mismatches 32; Indels 3; Gaps 1;

QY 1 QVTLKESGPGILOPSTLSITCSFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 60
Db 20 QVQLQESGPGILVFPSETLSLCTVSGGISSTNYVWIRQPPKLEWIGSLNHSY 79
QY 61 YNPSLKSRITISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAAYMDYWGQTSVTVS 120
Db 80 YNPSLKSRVITISVDTSKNQFSLSLSSVTAADTAVYTCAR---LGMGAFDFWGHGTWTVS 136
QY 121 S 121
Db 137 S 137

RESULT 14
Q9UL75 PRELIMINARY; PRT; 122 AA.
AC Q9UL75;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; PubMed=9614934;
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Search completed: January 14, 2004, 19:13:12
Job time : 40.6667 secs

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RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035039; AAD56275.1; -.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 13719 MW; 56CB0612586A6529 CRC64;

Query Match 52.4%; Score 331.5; DB 4; Length 122;
Best Local Similarity 54.4%; Pred. No. 18-28; 32; Indels 7; Gaps 3;
Matches 68; Conservative 18; Mismatches 32; Indels 7; Gaps 3;

QY 1 QVTLKESGPGILQPSQTLSTLTCFSGFSLSSTGGMVSWIRQSPGKLEWLAHIY----WD 56
Db ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
1 QVQLQSGPGLVKPKSTLSTLCAISGDSVSSNAANWIRQSPGKLEWIGRTYYRSKWY 60

QY 57 DDKRYNPISLKSRLTISKOTSSNOVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQTS 116
Db ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
61 ND--YRVSVKSRITINPDTSRKNQSLNLSVTPEDTAVYYCARDLELLG-QPDYWGQGT 117

QY 117 VTVSS 121
Db |||||

QY 118 VTVSS 122
Db |||||

RESULT 15
Q81ZD7 PRELIMINARY; PRT; 130 AA.
AC Q81ZD7;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DE Anti-thyroglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Jang Y.-J., Chung J., Park J.-Y.;
RT "Isolation and Sequence Analysis of Monoclonal Anti-Histone and Anti-
RT Thyroglobulin Single Chain Fv from SLE Patient by Phage Display.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY145445; AN64329.1; -.
FT NON_TER 1
FT NON_TER 130
SQ SEQUENCE 130 AA; 13901 MW; 036131FC6EC1551E CRC64;

Query Match 48.6%; Score 307.5; DB 4; Length 130;
Best Local Similarity 50.0%; Pred. No. 4.8e-26;
Matches 85; Conservative 20; Mismatches 36; Indels 9; Gaps 3;

QY 1 QVTLKESGPGILQPSQTLSTLTCFSGFSLSSTGGMVSWIRQSPGKLEWLAHIY----W 55
Db ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
1 QVQLQSGPGLVKPKSTLSTLTCVSGSISSSSYWGWIRQSPGKLEWIGSLYSGSTY 60

QY 56 DDKRYNPISLKSRLTISKOTSSNOVFLKITSVDTRDTATYYCARRVSLT---AYA-MDYW 111
Db ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
61 SGSPYAPSRVRSRIISVDTSKNQLSLRSLSVTAADTAVYYCASPTHCSGGGCIYAFQHW 120

QY 112 GQSTSVTVSS 121
Db |||||

QY 121 GQGLVTVSS 130
Db |||||
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OM protein - protein search, using sw model

Run on: January 14, 2004, 19:10:12 ; Search time 15.1905 Seconds
(without alignments)
337.028 Million cell updates/sec

Title: US-09-759-112A-7

Perfect score: 633

Sequence: 1 QVTLKSEPGILQPSQTLSL.....SLTAYAMDYWGQGVTVVSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/prodata/2/1aa/5A_COMB.pep.*
- 2: /cgn2_6/prodata/2/1aa/53_COMB.pep.*
- 3: /cgn2_6/prodata/2/1aa/5A_COMB.pep.*
- 4: /cgn2_6/prodata/2/1aa/53_COMB.pep.*
- 5: /cgn2_6/prodata/2/1aa/5A_COMB.pep.*
- 6: /cgn2_6/prodata/2/1aa/53_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	569	89.9	140	2	US-08-483-636-4
2	569	89.9	140	2	US-08-483-632-4
3	569	89.9	141	2	US-08-483-636-10
4	569	89.9	141	2	US-08-483-632-10
5	567.5	89.7	246	1	US-08-197-834-7
6	551.5	87.1	122	1	US-08-436-463-14
7	522.5	82.5	139	5	PCT-US95-07372-10
8	521.5	82.4	120	2	US-08-553-501A-88
9	521.5	82.4	120	3	US-09-205-231-88
10	521.5	82.4	139	3	US-08-553-501A-29
11	521.5	82.4	139	3	US-09-205-231-29
12	506.5	80.0	120	2	US-08-290-592E-32
13	505.5	79.9	143	1	US-08-436-463-2
14	504	79.6	108	1	US-08-436-463-17
15	502	79.3	141	2	US-08-483-632-12
16	502	79.3	141	2	US-08-483-636-12
17	500	79.0	121	2	US-08-483-636-64
18	500	79.0	121	2	US-08-483-632-64
19	499.5	78.9	120	5	PCT-US95-10053-29
20	499.5	78.9	120	5	PCT-US96-09448-32
21	499	78.8	108	1	US-08-436-463-15
22	489.5	77.3	120	5	PCT-US95-10053-28
23	489.5	77.3	120	5	PCT-US96-09448-31
24	482	76.1	114	1	US-08-436-463-16
25	470.5	74.3	126	4	US-09-225-322B-4
26	470.5	74.3	126	4	US-09-764-304-4
27	470.5	74.3	141	4	US-09-225-322B-2

28	470.5	74.3	141	4	US-09-764-304-2	Sequence 2, Appli
29	467.5	73.9	120	2	US-08-290-592B-31	Sequence 31, Appl
30	459.5	72.5	120	4	US-09-025-769B-23	Sequence 23, Appl
31	454	71.7	121	4	US-09-025-769B-37	Sequence 37, Appl
32	454	71.7	121	4	US-09-025-769B-61	Sequence 61, Appl
33	445	70.3	123	5	PCT-US95-10053-27	Sequence 27, Appl
34	445	70.3	123	5	PCT-US96-09448-30	Sequence 30, Appl
35	443	70.0	499	3	US-09-049-672A-1	Sequence 1, Appli
36	440.5	69.6	139	3	US-08-553-501A-59	Sequence 59, Appl
37	440.5	69.6	139	3	US-09-205-231-59	Sequence 59, Appl
38	437.5	69.1	139	2	US-08-553-501A-61	Sequence 61, Appl
39	437.5	69.1	139	3	US-09-205-231-61	Sequence 61, Appl
40	436	68.9	123	2	US-08-290-592B-30	Sequence 30, Appl
41	433.5	68.5	120	2	US-08-553-501A-90	Sequence 90, Appl
42	433.5	68.5	120	3	US-09-205-231-90	Sequence 90, Appl
43	431.5	68.2	141	2	US-08-345-321-10	Sequence 10, Appl
44	430.5	68.0	120	2	US-08-553-501A-91	Sequence 91, Appl
45	430.5	68.0	120	3	US-09-205-231-91	Sequence 91, Appl

ALIGNMENTS

RESULT 1
US-08-483-636-4
; Sequence 4, Application US/08483636
; Patent No. 5914110
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,636
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein

US-08-483-636-4

Query Match 89.9%; Score 569; DB 2; Length 140;
 Best Local Similarity 90.1%; Pred. No. 5.8e-50;
 Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 QY 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIROPSGKGLWLAHIYDDDKR 60
 DB 20 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIROPSGKGLWLAHIYDDDKR 79
 QY 61 YNPSLKSLRTISKDTSSNQVFLKITSVDTRTATYYCARRVSLTAYAMDYWGQGTSTVTVS 120
 DB 80 YNPSLKSLRTISKDTSSNQVFLKITSVDTRTATYYCARRVSLTAYAMDYWGQGTSTVTVS 139
 QY 121 S 121
 DB 140 S 140

RESULT 2

US-08-483-632-4
 ; Sequence 4, Application US/08483632
 ; Patent No. 5928904
 ; GENERAL INFORMATION:
 ; APPLICANT: Holmes, Stephen D.
 ; APPLICANT: Gross, Mitchell S.
 ; APPLICANT: Sylvester, Daniel R.
 ; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
 ; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
 ; NUMBER OF SEQUENCES: 75
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SmithKline Beecham Corp./Corporate
 ; ADDRESSEE: Intellectual Property
 ; STREET: P.O. Box 1539 / UW2220
 ; CITY: King of Prussia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19406-0939
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/483,632
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/117366
 ; FILING DATE: 07-SEP-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/136783
 ; FILING DATE: 14-OCT-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US/94/10308
 ; FILING DATE: 07-SEP-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sutton, Jeffrey A.
 ; REGISTRATION NUMBER: 34,028
 ; REFERENCE/DOCKET NUMBER: P50186-3
 ; TELEPHONE: (215) 270-5024
 ; TELEFAX: (215) 270-5090
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 140 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-483-632-4

Query Match 89.9%; Score 569; DB 2; Length 140;
 Best Local Similarity 90.1%; Pred. No. 5.8e-50;

Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIROPSGKGLWLAHIYDDDKR 60
 DB 20 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIROPSGKGLWLAHIYDDDKR 79
 QY 61 YNPSLKSLRTISKDTSSNQVFLKITSVDTRTATYYCARRVSLTAYAMDYWGQGTSTVTVS 120
 DB 80 YNPSLKSLRTISKDTSSNQVFLKITSVDTRTATYYCARRVSLTAYAMDYWGQGTSTVTVS 139
 QY 121 S 121
 DB 140 S 140

RESULT 3

US-08-483-636-10
 ; Sequence 10, Application US/08483636
 ; Patent No. 5914110
 ; GENERAL INFORMATION:
 ; APPLICANT: Holmes, Stephen D.
 ; APPLICANT: Gross, Mitchell S.
 ; APPLICANT: Sylvester, Daniel R.
 ; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
 ; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
 ; NUMBER OF SEQUENCES: 75
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SmithKline Beecham Corp./Corporate
 ; ADDRESSEE: Intellectual Property
 ; STREET: P.O. Box 1539 / UW2220
 ; CITY: King of Prussia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19406-0939
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/483,636
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/117366
 ; FILING DATE: 07-SEP-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/136783
 ; FILING DATE: 14-OCT-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US/94/10308
 ; FILING DATE: 07-SEP-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sutton, Jeffrey A.
 ; REGISTRATION NUMBER: 34,028
 ; REFERENCE/DOCKET NUMBER: P50186-3
 ; TELEPHONE: (215) 270-5024
 ; TELEFAX: (215) 270-5090
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 141 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-483-636-10

Query Match 89.9%; Score 569; DB 2; Length 141;
 Best Local Similarity 90.1%; Pred. No. 5.9e-50;
 Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIROPSGKGLWLAHIYDDDKR 60

Db 21 QVTLKESGPGILOPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYDDDKR 80
QY 61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMYWGQTSVTVS 120
Db 81 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVTFYWFYFDVWGAGITVTVS 140
QY 121 S 121
Db 141 S 141

RESULT 4

US-08-483-632-10
; Sequence 10, Application US/08483632
; Patent No. 5928904
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,632
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 141 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-483-632-10

Query Match 89.9%; Score 569; DB 2; Length 141;
Best Local Similarity 90.1%; Pred. No. 5.9e-50;
Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVTLKESGPGILOPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYDDDKR 60
Db 21 QVTLKESGPGILOPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYDDDKR 80
QY 61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMYWGQTSVTVS 120

Db 81 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVTFYWFYFDVWGAGITVTVS 140
QY 121 S 121
Db 141 S 141

RESULT 5

US-08-197-834-7
; Sequence 7, Application US/08197834
; Patent No. 5639455
; GENERAL INFORMATION:
; APPLICANT: SHIMAMURA, TOSHIRO
; APPLICANT: NAKAZAWA, HARUMI
; APPLICANT: HAMURO, JUNJI
; TITLE OF INVENTION: IMMUNOSUPPRESSANT
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,834
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 028173/1993
; FILING DATE: 17-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5639455man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-661-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-197-834-7

Query Match 89.7%; Score 567.5; DB 1; Length 246;
Best Local Similarity 89.6%; Pred. No. 1.1e-49;
Matches 112; Conservative 3; Mismatches 5; Indels 5; Gaps 2;

QY 1 QVTLKESGPGILOPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYDDDKR 60
Db 123 QVLEESGPGILOPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYDDDKH 182
QY 61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTA----YAMYWGQTS 116
Db 183 YNPSLKSRLTISKDTSTNQVFLAITSVDTRDTATYTCARR-SLYGNWGDYAMYWGQTS 241
QY 117 VTVSS 121
Db 242 VTVSS 246

RESULT 6

US-08-436-463-14
; Sequence 14, Application US/08436463

Patent No. 5760185
GENERAL INFORMATION:
APPLICANT: KIMACHI, Kazuhiko
APPLICANT: MAEDA, Hiroaki
APPLICANT: NISHIYAMA, Kiyoto
APPLICANT: TOKIYOSHI, Sachio
TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/436,463
FILING DATE: 26-JUN-1995
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 341255/1992
FILING DATE: 28-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: KIMACHI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
MOLECULE TYPE: protein
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MEDIUM TYPE: protein
US-08-436-463-14

Query Match 87.1%; Score 551.5; DB 1; Length 122;
Best Local Similarity 91.4%; Pred. No. 2.8e-48;
Matches 106; Conservative 2; Mismatches 7; Indels 1; Gaps 1;
QY 1 QVTLKESGPGILQPSQTLISLTCSFGSLSTSGMGVSWIRQPSGKLEWLAHIYWDGDKR 60
Db 8 QVTLKESGPGILQPSQTLISLTCSFGSLSTSGMGVSWIRQPSGKLEWLAHIYWDGDKR 67
QY 61 YNPISLKSRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQGT 116
Db 68 YNPISLKSRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQGT 122

RESULT 7
PCT-US95-07372-10
Sequence 10 Application PC/TUS9507372
GENERAL INFORMATION:
APPLICANT: Oklahoma Medical Research Foundation
TITLE OF INVENTION: Calcium Binding Recombinant
TITLE OF INVENTION: Antibody Against Protein C
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07372
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF106CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: HPC-4 Heavy Chain Variable Region (VH Gamma)
FEATURE:
NAME/KEY: misc feature
LOCATION: 20..139
OTHER INFORMATION: /note= "Gln at position 20 starts mature peptide."
PCT-US95-07372-10

Query Match 82.5%; Score 522.5; DB 5; Length 139;
Best Local Similarity 84.3%; Pred. No. 2.7e-45;
Matches 102; Conservative 3; Mismatches 15; Indels 1; Gaps 1;
QY 1 QVTLKESGPGILQPSQTLISLTCSFGSLSTSGMGVSWIRQPSGKLEWLAHIYWDGDKR 60
Db 20 QVTLKESGPGILQPSQTLISLTCSFGSLSTSGMGVSWIRQPSGKLEWLAHIYWDGDKR 79
QY 61 YNPISLKSRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQGT 120
Db 80 YNPISLKSRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQGT 138
QY 121 S 121
Db 139 S 139

RESULT 8
US-08-553-501A-88
Sequence 88 Application US/08553501A
Patent No. 5856135
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: HIRATA, Yuichi
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/553,501A
/ FILING DATE: 20-FEB-1996
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: WO PCT/JP94/00859
/ FILING DATE: 30-MAY-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 5-129787
/ FILING DATE: 31-MAY-1993
/ NAME: WEGNER, Harold C.
/ REGISTRATION NUMBER: 25,258
/ REFERENCE/DOCKET NUMBER: 53466/177/AAOK
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202)672-5300
/ TELEFAX: (202)672-5399
/ TELEX: 904136
/ INFORMATION FOR SEQ ID NO: 88:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 120 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-553-501A-88

Query Match 82.4%; Score 521.5; DB 2; Length 120;
Best Local Similarity 83.7%; Pred. No. 2.8e-45;
Matches 103; Conservative 6; Mismatches 9; Indels 5; Gaps 2;

QY 1 QVTLKESGPGILQPSQTLSTLTCFSFGSLSTSGMGVSWIRQPSGKLEWLAHIYWDKDKR 60
Db 1 QVTLKESGPGILQPSQTLSTLTCFSFGSLSTSGMGVSWIRQPSGKLEWLAHIWWDKDY 60

QY 61 YNPALKRLTISKDTSSNQVFLKITSVDTRDTATYYCARVSLTAY--AMDYWGQGTSTV 118
Db 61 YNPALKGRITISKDTSSNQVFLKIASVTADTATYYCAR---MEDYDEAMDYWGQGTSTV 117

QY 119 VSS 121
Db 118 VSS 120

RESULT 9
US-09-205-231-88
/ Sequence 88, Application US/09205231
/ Patent No. 6121423
/ GENERAL INFORMATION:
/ APPLICANT: TSUCHIYA, Masayuki
/ APPLICANT: SATO, Koh
/ TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
/ TITLE OF INVENTION: INTERLEUKIN-6
/ NUMBER OF SEQUENCES: 91
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Foley & Lardner
/ STREET: 3000 K Street, N.W., Suite 500
/ City: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20007-5109
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/205,231
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US/08/553,501
/ FILING DATE: 20-FEB-1996
/ APPLICATION NUMBER: WO PCT/JP94/00859
/ FILING DATE: 30-MAY-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 5-129787
/ FILING DATE: 31-MAY-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: WEGNER, Harold C.
/ REGISTRATION NUMBER: 25,258
/ REFERENCE/DOCKET NUMBER: 53466/177/AAOK
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202)672-5300
/ TELEFAX: (202)672-5399
/ TELEX: 904136
/ INFORMATION FOR SEQ ID NO: 88:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 120 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-09-205-231-88

Query Match 82.4%; Score 521.5; DB 3; Length 120;
Best Local Similarity 83.7%; Pred. No. 2.8e-45;
Matches 103; Conservative 6; Mismatches 9; Indels 5; Gaps 2;

QY 1 QVTLKESGPGILQPSQTLSTLTCFSFGSLSTSGMGVSWIRQPSGKLEWLAHIYWDKDKR 60
Db 1 QVTLKESGPGILQPSQTLSTLTCFSFGSLSTSGMGVSWIRQPSGKLEWLAHIWWDKDY 60

QY 61 YNPALKRLTISKDTSSNQVFLKITSVDTRDTATYYCARVSLTAY--AMDYWGQGTSTV 118
Db 61 YNPALKGRITISKDTSSNQVFLKIASVTADTATYYCAR---MEDYDEAMDYWGQGTSTV 117

QY 119 VSS 121
Db 118 VSS 120

RESULT 10
US-08-553-501A-29
/ Sequence 29, Application US/08553501A
/ Patent No. 5858135
/ GENERAL INFORMATION:
/ APPLICANT: TSUCHIYA, Masayuki
/ APPLICANT: SATO, Koh
/ APPLICANT: HIRATA, Yuichi
/ TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
/ TITLE OF INVENTION: INTERLEUKIN-6
/ NUMBER OF SEQUENCES: 91
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Foley & Lardner
/ STREET: 3000 K Street, N.W., Suite 500
/ City: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20007-5109
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/553,501A
/ FILING DATE: 20-FEB-1996
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: WO PCT/JP94/00859
/ FILING DATE: 30-MAY-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 5-129787
/ FILING DATE: 31-MAY-1993

```

; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/177/AOOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-553-501A-29
;
; Query Match 82.4%; Score 521.5; DB 2; Length 139;
; Best Local Similarity 83.7%; Pred. No. 3.4e-45;
; Matches 103; Conservative 6; Mismatches 9; Indels 5; Gaps 2;
;
; QY 1 QVTLKESGPGILQPSQTLTLTCSFSGFSLSTSGMGVSWIROPQSGKLEWLAIHWDDDKR 60
; Db 20 QVTLKESGPGILQPSQTLTLTCSFSGFSLSTSGMGVSWIROPQSGKLEWLAIHWDDDKY 79
;
; QY 61 YNPSLKSLRTISKDTSSNQVFLKITSVTRDTATYTCARRVSLTAY--AMDYWGQGTSTV 118
; Db 80 YNPALKGRLTISKDTSSNQVFLKIASVVTADTATYTCAR---MEDYDEAMDYWGQGTSTV 136
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; QY 119 VSS 121
; Db 137 VSS 139
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; RESULT 11
; US-09-205-231-29
; Sequence 29, Application US/09205231
; Patent No. 6121423
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SAITO, Koh
; APPLICANT: HIRATA, Yuichi
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/205,231
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,501
; FILING DATE: 20-FEB-1996
; APPLICATION NUMBER: WO PCT/JP94/00859
; FILING DATE: 30-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-129787
; FILING DATE: 31-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/177/AOOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-553-501A-29
;
; Query Match 82.4%; Score 521.5; DB 2; Length 139;
; Best Local Similarity 83.7%; Pred. No. 3.4e-45;
; Matches 103; Conservative 6; Mismatches 9; Indels 5; Gaps 2;
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; QY 1 QVTLKESGPGILQPSQTLTLTCSFSGFSLSTSGMGVSWIROPQSGKLEWLAIHWDDDKR 60
; Db 20 QVTLKESGPGILQPSQTLTLTCSFSGFSLSTSGMGVSWIROPQSGKLEWLAIHWDDDKY 79
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; QY 61 YNPSLKSLRTISKDTSSNQVFLKITSVTRDTATYTCARRVSLTAY--AMDYWGQGTSTV 118
; Db 80 YNPALKGRLTISKDTSSNQVFLKIASVVTADTATYTCAR---MEDYDEAMDYWGQGTSTV 136
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; QY 119 VSS 121
; Db 137 VSS 139
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; RESULT 12
; US-08-290-592E-32
; Sequence 32, Application US/08290592E
; Patent No. 5824307
; GENERAL INFORMATION:
; APPLICANT: JOHNSON, L.
; TITLE OF INVENTION: Human Murine Chimeric Antibodies Against
; TITLE OF INVENTION: Respiratory Syncytial Virus
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI, STEWART &
; ADDRESSEE: OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290,592E
; FILING DATE: August 15, 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/813,372
; FILING DATE: December 23, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 469201-257
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 AMINO ACIDS
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; US-08-290-592E-32
;
; Query Match 80.0%; Score 506.5; DB 2; Length 120;

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Best Local Similarity 81.8%; Pred. No. 9.1e-44;
Matches 99; Conservative 7; Mismatches 14; Indels 1; Gaps 1;
QY 1 QVTLKESGPGILQPSQTLSTLTCFSFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 60
DB 1 QVELQESGPGILQPSQTLSTLTCFSFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKD 60
QY 61 YNPSLKRSLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQTSVTYS 120
DB 61 YNPSLKRSLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQTSVTYS 119
QY 121 S 121
DB 120 S 120
RESULT 13
US-08-436-463-2
; Sequence 2, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: NISHIYAMA, Kiyoto
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,463
; FILING DATE: 26-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 341255/1992
; FILING DATE: 28-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: KIMACHI=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 143 amino acids
; TYPE: amino acid
; STRANDEDNESS: linear
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-436-463-2
Query Match 79.9%; Score 505.5; DB 1; Length 143;
Best Local Similarity 79.8%; Pred. No. 1.4e-43;
Matches 99; Conservative 6; Mismatches 16; Indels 3; Gaps 1;
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DB 20 QVTLKESGPGILQPSQTLSTLTCFSFSLSTSGMGAGWIRQPSGKLEWLAIHYWDDDKR 79
QY 61 YNPSLKRSLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQTSV 117
DB 80 YNPSLKRSLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQTSV 139

QY 118 TVSS 121
DB 140 TVSA 143
RESULT 14
US-08-436-463-17
; Sequence 17, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: NISHIYAMA, Kiyoto
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,463
; FILING DATE: 26-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 341255/1992
; FILING DATE: 28-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: KIMACHI=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-436-463-17
Query Match 79.6%; Score 504; DB 1; Length 108;
Best Local Similarity 90.8%; Pred. No. 1.4e-43;
Matches 99; Conservative 1; Mismatches 7; Indels 2; Gaps 2;
QY 9 PGILQPSQTLSTLTCFSFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKRYNPSLKSR 68
DB 1 PGILQPSQTLSTLTCFSFSLSTSGMG-SWIRQPSGKLEWLAIHYWDDDKRYNPSLKSR 59
QY 69 LTISKDTSSNQVFLKITSVDTRDTATYTCARRV-SLTAYAMDYWGQTS 116
DB 60 LTISKDTSSNQVFLKITSVDTRDTATYTCARRV-SLTAYAMDYWGQTS 108
RESULT 15
US-08-483-636-12
; Sequence 12, Application US/08483636
; Patent No. 5914110
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.

APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSER: SmithKline Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STREET: P.O. Box 1539 / UW2220
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,636
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5030
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-636-12

Query Match 79.3%; Score 502; DB 2; Length 141;
Best Local Similarity 76.9%; Pred. No. 3.1e-43;
Matches 93; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

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QY	61	YNPSLKSRLTISKOTSNOVFLKITSVDTRDTATYYCAERVSILTAYAMDYWGQGTSTVTS	120
Db	81	YNPSLKSRLTISKOTSNOVFLKITSVDTRDTATYYCAERVTVFYWFYFDVWGGRGTPVTS	140
QY	121	S	121
Db	141	S	141

Search completed: January 14, 2004, 19:14:23
Job time : 16.1905 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 14, 2004, 19:13:23 ; Search time 169.19 Seconds
(without alignments)
146.239 Million cell updates/sec

Title: US-09-759-112a-7

Perfect score: 633

Sequence: 1 QVTLKESGFIQPSQTLSTL.....SLTAYAMDYWGQTSVTVS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 762491 seqs, 20448190 residues

Total number of hits satisfying chosen parameters: 762491

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match %	Score	Length	DB ID	Description
1	633	100.0	121	11	US-09-759-112a-7
2	569	89.9	140	10	US-09-879-461-4
3	569	89.9	141	10	US-09-879-461-10
4	555	87.7	123	11	US-09-995-529-12
5	551	87.0	142	12	US-10-010-942B-16
6	525	82.9	119	12	US-10-323-903-3
7	506.5	80.0	120	10	US-09-158-120A-32
8	506.5	80.0	143	9	US-09-881-823-8
9	502	79.3	141	10	US-09-879-461-12
10	498.5	78.9	120	15	US-10-011-331-3
11	470.5	74.3	126	9	US-09-764-304-4
12	470.5	74.3	126	12	US-10-166-626-4
13	470.5	74.3	126	15	US-10-265-713-4
14	470.5	74.3	141	9	US-09-764-304-2
15	470.5	74.3	141	12	US-10-166-626-2

16	470.5	74.3	141	15	US-10-265-713-2	Sequence 2, Appli
17	468.5	74.0	120	9	US-09-796-848A-4	Sequence 4, Appli
18	468.5	74.0	120	10	US-09-771-415-2	Sequence 2, Appli
19	468.5	74.0	450	10	US-09-996-288-208	Sequence 208, App
20	468.5	74.0	450	11	US-09-996-265-208	Sequence 208, App
21	467.5	73.9	120	10	US-09-158-120A-31	Sequence 31, Appl
22	466.5	73.7	120	10	US-09-771-415-18	Sequence 18, Appl
23	466.5	73.7	120	10	US-09-771-415-24	Sequence 20, Appl
24	466.5	73.7	120	10	US-09-771-415-24	Sequence 24, Appl
25	466.5	73.7	120	10	US-09-771-415-26	Sequence 26, Appl
26	466.5	73.7	450	10	US-09-996-288-210	Sequence 210, App
27	466.5	73.7	450	10	US-09-996-288-240	Sequence 240, App
28	466.5	73.7	450	11	US-09-996-265-210	Sequence 210, App
29	466.5	73.7	450	11	US-09-996-265-240	Sequence 240, App
30	465.5	73.5	450	10	US-09-996-288-238	Sequence 238, App
31	465.5	73.5	450	10	US-09-996-288-242	Sequence 242, App
32	465.5	73.5	450	10	US-09-996-288-244	Sequence 244, App
33	465.5	73.5	450	10	US-09-996-288-246	Sequence 246, App
34	465.5	73.5	450	11	US-09-996-285-238	Sequence 238, App
35	465.5	73.5	450	11	US-09-996-265-242	Sequence 242, App
36	465.5	73.5	450	11	US-09-996-265-244	Sequence 244, App
37	465.5	73.5	450	11	US-09-996-265-246	Sequence 246, App
38	464.5	73.4	120	10	US-09-771-415-22	Sequence 22, Appl
39	463.5	73.2	450	10	US-09-996-288-248	Sequence 248, App
40	463.5	73.2	450	11	US-09-996-285-248	Sequence 248, App
41	463	73.1	119	12	US-10-156-255-7	Sequence 7, Appli
42	462.5	73.1	120	9	US-09-796-848A-2	Sequence 2, Appli
43	462.5	73.1	120	10	US-09-996-288-7	Sequence 7, Appli
44	462.5	73.1	120	11	US-09-996-265-7	Sequence 7, Appli
45	462.5	73.1	120	12	US-10-020-354-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1

US-09-759-112a-7
; Sequence 7, Application US/09759112a
; Publication No. US20030100741A1
; GENERAL INFORMATION:
; APPLICANT: Mueller, Sybille
; APPLICANT: Kohler, Heinz
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING VARIABLE REGIONS OF HEAVY AND LIGHT
; TITLE OF INVENTION: OF MONOCLONAL ANTIBODY 1F7, AN ANTI-IDIOTYPIC ANTIBODY REACTIVE
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 200-013
; CURRENT APPLICATION NUMBER: US/09/759,112A
; CURRENT FILING DATE: 2001-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; TYPE: PRT
; ORGANISM: mouse
; US-09-759-112a-7

Query Match 100.0%; Score 633; DB 11; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.3e-54;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVTLKESGFIQPSQTLSTLCTCSFGSLSTSGMGVSWIRQPSGKGLWLAHIYDDDKR 60
DB 1 QVTLKESGFIQPSQTLSTLCTCSFGSLSTSGMGVSWIRQPSGKGLWLAHIYDDDKR 60
QY 61 YNPSLKSLRTISKDSSNOVFLKITSVTRDTRATYYCARRVSLTAYAMDYWGQTSVTVS 120
DB 61 YNPSLKSLRTISKDSSNOVFLKITSVTRDTRATYYCARRVSLTAYAMDYWGQTSVTVS 120
QY 121 S 121
DB 121 S 121

RESULT 2

US-09-879-461-4
; Sequence 4, Application US/09879461
; Publication No. US20020193575A1
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; Gross, Mitchell S.
; Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: Corporate Intellectual Property, UW2220 - 709
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/879,461
; FILING DATE: 12-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/612,929
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/136,783
; FILING DATE: 14-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-879-461-4

Query Match 89.9%; Score 569; DB 10; Length 140;
Best Local Similarity 90.1%; Pred. No. 2.8e-48;
Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
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Db 20 QVTLKESGFGILQPSQTLTSLTCSFGSFLSTSGMGVSWIRQPSGKLEWLAHIYWDGDKR 79
QY 61 YNPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGCGTSVTVS 120
Db 80 YNPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGCGTSVTVS 139
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Db 140 S 140

RESULT 3

US-09-879-461-10
; Sequence 10, Application US/09879461
; Publication No. US20020193575A1
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; Gross, Mitchell S.

; Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: Corporate Intellectual Property, UW2220 - 709
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/879,461
; FILING DATE: 12-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/612,929
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/136,783
; FILING DATE: 14-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 141 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-879-461-10
Query Match 89.9%; Score 569; DB 10; Length 141;
Best Local Similarity 90.1%; Pred. No. 2.8e-48;
Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
QY 1 QVTLKESGFGILQPSQTLTSLTCSFGSFLSTSGMGVSWIRQPSGKLEWLAHIYWDGDKR 60
Db 21 QVTLKESGFGILQPSQTLTSLTCSFGSFLSTSGMGVSWIRQPSGKLEWLAHIYWDGDKR 80
QY 61 YNPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGCGTSVTVS 120
Db 81 YNPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGCGTSVTVS 140
QY 121 S 121
Db 141 S 141
RESULT 4
US-09-995-529-12
; Sequence 12, Application US/09995529
; Publication No. US20030099655A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; Related Methods
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 123
TYPE: PRT
ORGANISM: Mus musculus
US-09-995-529-12

Query Match 87.7%; Score 555; DB 11; Length 123;
Best Local Similarity 87.8%; Pred. No. 5.7e-47;
Matches 108; Conservative 5; Mismatches 8; Indels 2; Gaps 1;

QY 1 QVTLKESGPGILQPSOTLSLTCFSFGSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 60
Db 1 QVTLKETGPGILQPSOTLSLTCFSFGSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 60
QY 61 YNPSLKSLRTISKDTSSNQVFLKITSVDTRDTATYTCARRVSL--TAYANDYWGQTSVT 118
Db 61 YNPSLKSLRTISKDTSSNQVFLKITSVDTRDTATYTCARRVSGPYANDYWGQTSVT 120
QY 119 VSS 121
Db 121 VSS 123

RESULT 5

US-10-010-942B-16
Sequence 16, Application US/10010942B
Publication No. US20030165496A1

GENERAL INFORMATION:
APPLICANT: Basi, Gurik
APPLICANT: Saldanha, Jose
APPLICANT: Vednock, Ted
TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
FILE REFERENCE: ELN-002
CURRENT APPLICATION NUMBER: US/10/010,942B
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: US 60/251,892
PRIOR FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 63
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16
LENGTH: 142
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(19)
US-10-010-942B-16

Query Match 87.0%; Score 551; DB 12; Length 142;
Best Local Similarity 87.8%; Pred. No. 1.7e-46;
Matches 108; Conservative 1; Mismatches 12; Indels 2; Gaps 1;
QY 1 QVTLKESGPGILQPSOTLSLTCFSFGSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 60
Db 20 QATLKESGPGILQSSOTLSLTCFSFGSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 79
QY 61 YNPSLKSLRTISKDTSSNQVFLKITSVDTRDTATYTCARR--VSLTAYANDYWGQTSVT 118
Db 80 YNPSLKSLRTISKDTSSNQVFLKITSVDTRDTATYTCARRPITPVLVDANDYWGQTSVT 139
QY 119 VSS 121
Db 140 VSS 142

RESULT 6

US-10-323-903-3
Sequence 3, Application US/10323903
Publication No. US2003022832A1
GENERAL INFORMATION:
APPLICANT: FISCHER, GERALD WALTER

APPLICANT: SCHUMAN, RICHARD F.
APPLICANT: MOND, JAMES JACOB
APPLICANT: KOKAI-KUN, JOHN FITZGERALD
APPLICANT: FOSTER, SIMON
APPLICANT: STINSON, JEFFREY R.
TITLE OF INVENTION: MULTIFUNCTIONAL MONOCLONAL ANTIBODIES DIRECTED TO
FILE REFERENCE: 07787,0059
CURRENT APPLICATION NUMBER: US/10/323,903
CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: 60/343,444
PRIOR FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/097,055
PRIOR FILING DATE: 1998-06-15
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 119
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic M130
OTHER INFORMATION: heavy chain antibody
US-10-323-903-3

Query Match 82.9%; Score 525; DB 12; Length 119;
Best Local Similarity 83.1%; Pred. No. 4.8e-44;
Matches 103; Conservative 5; Mismatches 8; Indels 8; Gaps 2;
QY 1 QVTLKESGPGILQPSOTLSLTCFSFGSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 60
Db 1 QVQLQSGPGILQPSQTLSTLTCFSFGSLSTSGMSVSWIRQPSGKLEWLAIHYWDDDKR 60
QY 61 YNPSLKSLRTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAND---YWGQTSV 117
Db 61 YNPSLKSLRTISKDTSSNQVFLKITSVDTRDTATYTCARRN-----YDIDWFVYWGQTLV 115
QY 118 TVSS 121
Db 116 TVSA 119

RESULT 7

US-09-158-120A-32
Sequence 32, Application US/09158120A
Patent No. US20020102257A1
GENERAL INFORMATION:
APPLICANT: JOHNSON, L.
TITLE OF INVENTION: Human Murine Chimeric Antibodies Against
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
ADDRESSEE: STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: P160
OPERATING SYSTEM: Windows95
SOFTWARE: MS Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/158,120A
FILING DATE: September 21, 1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290,592
FILING DATE: August 15, 1994
APPLICATION NUMBER: 07/813,372
FILING DATE: December 23, 1991

```
ATTORNEY/AGENT INFORMATION:
NAME: OIsteim, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 469201-367
TELECOMMUNICATION INFORMATION:
TELEPHONE: 973-994-1700
TELEFAX: 973-994-1744
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 AMINO ACIDS
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-09-158-120A-32

Query Match      80.0%; Score 506.5; DB 10; Length 120;
Best Local Similarity 81.8%; Pred. No. 3.2e-42;
Matches 99; Conservative 7; Mismatches 14; Indels 1; Gaps 1;

QY 1 QVTLKESGFGILQPSQTLTLCTCFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 60
DB 1 QVELQESGFGILQPSQTLTLCTCFSGFSLSTSGMGVSWIRQPSGEGLEWLADIWDDDKD 60
QY 61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQTSVTVS 120
DB 61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQTSVTVS 120
QY 121 S 121
DB 120 S 120

RESULT 8
US-09-881-823-8
Sequence 8, Application US/09881823
Patent No. US20020068066A1
GENERAL INFORMATION:
APPLICANT: SHI, WENYUAN
APPLICANT: ANDERSON, MAXWELL
APPLICANT: MORRISON, SHERIE
APPLICANT: TRINH, RYAN
APPLICANT: WIMS, LETITIA
APPLICANT: CHEN, LI
TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries
FILE REFERENCE: 22851-032
CURRENT APPLICATION NUMBER: US/09/881,823
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 07/378,577
PRIOR FILING DATE: 1999-08-20
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.0
SEQ ID NO 8
LENGTH: 143
TYPE: PRT
ORGANISM: Murine
US-09-881-823-8

Query Match      80.0%; Score 506.5; DB 9; Length 143;
Best Local Similarity 81.1%; Pred. No. 3.9e-42;
Matches 99; Conservative 7; Mismatches 15; Indels 1; Gaps 1;

QY 1 QVTLKESGFGILQPSQTLTLCTCFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 60
DB 20 QVTLKESGFGILQPSQTLTLCTCFSGFSLRTYIGVGNIRQPSGKLEWLAIHWNDNKY 79
QY 61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAY-AMDYWGQTSVTV 119
DB 80 YNTVLKSRLTISKDTSSNQVFLKIASVDTRDTATYTCARRVSLTAY-AMDYWGQTSVTV 139
QY 120 SS 121
DB 140 SS 141
```

```
RESULT 9
US-09-879-461-12
Sequence 12, Application US/09879461
Publication No. US20020193575A1
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
Gross, Mitchell S.
Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: Corporate Intellectual Property, UW2220 - 709
Swedeland Rd.
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,461
FILING DATE: 12-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/612,929
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/136,783
FILING DATE: 14-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-879-461-12

Query Match      79.3%; Score 502; DB 10; Length 141;
Best Local Similarity 76.3%; Pred. No. 1.1e-41;
Matches 93; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

QY 1 QVTLKESGFGILQPSQTLTLCTCFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 60
DB 21 QVTLKESGFGILQPSQTLTLCTCFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 80
QY 61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQTSVTVS 120
DB 81 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQTSVTVS 140
QY 121 S 121
DB 141 S 141

RESULT 10
US-10-011-931-3
Sequence 3, Application US/10011931
Publication No. US20030026806A1
GENERAL INFORMATION:
APPLICANT: WITTE, ALISON
```

```

; APPLICANT: VARNUM, BRIAN C.
; APPLICANT: QIAN, ZUEMING
; APPLICANT: VEZINA, CHRIS
; TITLE OF INVENTION: ANTIBODIES AND OTHER SELECTIVE IL-1 BINDING AGENTS THAT ALLOW BINDING TO IL-1 RECEPTOR BUT NOT ACTIVATION THEREOF
; FILE REFERENCE: A-731
; CURRENT APPLICATION NUMBER: US/10/011,931
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 60/244,118
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-011-931-3

Query Match      78.9%; Score 499.5; DB 15; Length 120;
Best Local Similarity 81.0%; Pred. No. 1.5e-41;
Matches 98; Conservative 9; Mismatches 13; Indels 1; Gaps 1;

QY 1 QVTLKESGPGILQPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDGDKR 60
DB 1 QVTLKESGPGILQPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDGDES 60
QY 61 YNPSLKSLRLTISKDTSSNQVFLKITSVTRDTATYTCARRVSLTAYAMDYMGQGTSTVTS 120
DB 61 YNPSLKSLRLTISKDTSSNQVFLKITSVTRDTATYTCARRVSLTAYAMDYMGQGTSTVTS 120
QY 121 S 121
DB 120 S 120

RESULT 11
US-09-764-304-4
; Sequence 4, Application US/09764304
; Patent No. US20020026036A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KIWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; CURRENT FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER FILING DATE: 1999-01-05
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Rat hybridoma
US-09-764-304-4

Query Match      74.3%; Score 470.5; DB 9; Length 126;
Best Local Similarity 75.4%; Pred. No. 1.1e-38;
Matches 92; Conservative 9; Mismatches 20; Indels 1; Gaps 1;

QY 1 QVTLKESGPGILQPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDGDKR 60
DB 5 QVTLKESGPGILQPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSGKGLEWLANVWSDAKY 64
QY 61 YNPSLKSLRLTISKDTSSNQVFLKITSVTRDTATYTCARRVSLTA-YAMDYMGQGTSTVTV 119
DB 65 YNPSLKSLRLTISKDTSSNQVFLKITSVTRDTATYTCARRVSLTA-YAMDYMGQGTSTVTV 124
QY 120 SS 121
DB 125 SS 126

RESULT 12
US-10-166-626-4
; Sequence 4, Application US/10166626
; Publication No. US20030166876A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KIWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166,626
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Rat hybridoma
US-10-166-626-4

Query Match      74.3%; Score 470.5; DB 12; Length 126;
Best Local Similarity 75.4%; Pred. No. 1.1e-38;
Matches 92; Conservative 9; Mismatches 20; Indels 1; Gaps 1;

QY 1 QVTLKESGPGILQPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDGDKR 60
DB 5 QVTLKESGPGILQPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSGKGLEWLANVWSDAKY 64
QY 61 YNPSLKSLRLTISKDTSSNQVFLKITSVTRDTATYTCARRVSLTA-YAMDYMGQGTSTVTV 119
DB 65 YNPSLKSLRLTISKDTSSNQVFLKITSVTRDTATYTCARRVSLTA-YAMDYMGQGTSTVTV 124
QY 120 SS 121
DB 125 SS 126

RESULT 13
US-10-265-713-4
; Sequence 4, Application US/10265713
; Publication No. US20030095964A1
; GENERAL INFORMATION:
```

```

Matches 92; Conservative 9; Mismatches 20; Indels 1; Gaps 1;

QY 1 QVTLKESGPGILQPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDGDKR 60
DB 5 QVTLKESGPGILQPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSGKGLEWLANVWSDAKY 64
QY 61 YNPSLKSLRLTISKDTSSNQVFLKITSVTRDTATYTCARRVSLTA-YAMDYMGQGTSTVTV 119
DB 65 YNPSLKSLRLTISKDTSSNQVFLKITSVTRDTATYTCARRVSLTA-YAMDYMGQGTSTVTV 124
QY 120 SS 121
DB 125 SS 126

RESULT 12
US-10-166-626-4
; Sequence 4, Application US/10166626
; Publication No. US20030166876A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KIWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166,626
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Rat hybridoma
US-10-166-626-4

Query Match      74.3%; Score 470.5; DB 12; Length 126;
Best Local Similarity 75.4%; Pred. No. 1.1e-38;
Matches 92; Conservative 9; Mismatches 20; Indels 1; Gaps 1;

QY 1 QVTLKESGPGILQPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDGDKR 60
DB 5 QVTLKESGPGILQPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSGKGLEWLANVWSDAKY 64
QY 61 YNPSLKSLRLTISKDTSSNQVFLKITSVTRDTATYTCARRVSLTA-YAMDYMGQGTSTVTV 119
DB 65 YNPSLKSLRLTISKDTSSNQVFLKITSVTRDTATYTCARRVSLTA-YAMDYMGQGTSTVTV 124
QY 120 SS 121
DB 125 SS 126

RESULT 13
US-10-265-713-4
; Sequence 4, Application US/10265713
; Publication No. US20030095964A1
; GENERAL INFORMATION:
```

APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUMANA, YOSHITSA
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/10/265,713
PRIOR FILING DATE: 2002-10-08
PRIOR APPLICATION NUMBER: US/09/225,322
PRIOR FILING DATE: 1999-01-05
PRIOR APPLICATION NUMBER: US 08/454,680
PRIOR FILING DATE: 1995-05-31
PRIOR APPLICATION NUMBER: US 08/408,133
PRIOR FILING DATE: 1995-03-21
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR FILING DATE: 1994-08-17
PRIOR APPLICATION NUMBER: US07/947,674
PRIOR FILING DATE: 1992-09-17
PRIOR APPLICATION NUMBER: JP 3-238375
PRIOR FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 126
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Rat hybridoma
US-10-265-713-4

Query Match 74.3%; Score 470.5; DB 15; Length 126;
Best Local Similarity 75.4%; Pred. No. 1.1e-38;
Matches 92; Conservative 9; Mismatches 20; Indels 1; Gaps 1;
QY 1 QVTLKESGPGILQPSQTLTLTCSFGSFLSTSGMGVSWIRQPSGKGLWLAHIYWDKDKR 60
DB 5 QVTLKESGPGILQPSQTLTLTCSFGSFLSTSGMGVSWIRQPSGKGLWLAHIYWDKDKR 64
QY 61 YNPSLKSLRTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTA-YANDYWGQGTSTVT 119
DB 65 YNPSLKSLRTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTA-YANDYWGQGTSTVT 124
QY 120 SS 121
DB 125 SS 126

RESULT 14
US-09-764-304-2
Sequence 2, Application US/09764304
Patent No. US20020026036A1
GENERAL INFORMATION:
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUMANA, YOSHITSA
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/09/764,304
PRIOR FILING DATE: 2001-01-19
EARLIER APPLICATION NUMBER: 09/225,322
EARLIER FILING DATE: 1999-01-05
EARLIER APPLICATION NUMBER: US 08/454,680
EARLIER FILING DATE: 1995-05-31
EARLIER APPLICATION NUMBER: US 08/408,133
EARLIER FILING DATE: 1995-03-21
EARLIER APPLICATION NUMBER: US 08/292,178
EARLIER FILING DATE: 1994-08-17
EARLIER APPLICATION NUMBER: US07/947,674
EARLIER FILING DATE: 1992-09-17
EARLIER APPLICATION NUMBER: JP 3-238375

EARLIER FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 141
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Rat hybridoma
US-09-764-304-2

Query Match 74.3%; Score 470.5; DB 9; Length 141;
Best Local Similarity 75.4%; Pred. No. 1.3e-38;
Matches 92; Conservative 9; Mismatches 20; Indels 1; Gaps 1;
QY 1 QVTLKESGPGILQPSQTLTLTCSFGSFLSTSGMGVSWIRQPSGKGLWLAHIYWDKDKR 60
DB 20 QVTLKESGPGILQPSQTLTLTCSFGSFLSTSGMGVSWIRQPSGKGLWLAHIYWDKDKR 79
QY 61 YNPSLKSLRTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTA-YANDYWGQGTSTVT 119
DB 80 YNPSLKSLRTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTA-YANDYWGQGTSTVT 139
QY 120 SS 121
DB 140 SS 141

RESULT 15
US-10-166-626-2
Sequence 2, Application US/10166626
Publication No. US20030166876A1
GENERAL INFORMATION:
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUMANA, YOSHITSA
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/10/166,626
CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: US/09/225,322B
PRIOR FILING DATE: 1999-01-05
PRIOR APPLICATION NUMBER: US 08/454,680
PRIOR FILING DATE: 1995-05-31
PRIOR APPLICATION NUMBER: US 08/408,133
PRIOR FILING DATE: 1995-03-21
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR FILING DATE: 1994-08-17
PRIOR APPLICATION NUMBER: US07/947,674
PRIOR FILING DATE: 1992-09-17
PRIOR APPLICATION NUMBER: JP 3-238375
PRIOR FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 141
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Rat hybridoma
US-10-166-626-2

Query Match 74.3%; Score 470.5; DB 12; Length 141;
Best Local Similarity 75.4%; Pred. No. 1.3e-38;
Matches 92; Conservative 9; Mismatches 20; Indels 1; Gaps 1;
QY 1 QVTLKESGPGILQPSQTLTLTCSFGSFLSTSGMGVSWIRQPSGKGLWLAHIYWDKDKR 60
DB 20 QVTLKESGPGILQPSQTLTLTCSFGSFLSTSGMGVSWIRQPSGKGLWLAHIYWDKDKR 79
QY 61 YNPSLKSLRTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTA-YANDYWGQGTSTVT 119

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 14, 2004, 15:52:50 : Search time 1621.9 Seconds
(without alignments)
8323.656 Million cell updates/sec

Title: US-09-759-112a-22

Perfect score: 330

Sequence: 1 gacattgtgctcaccaattc.....ggaccaagctgagctgaaa 330

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:

1: gb_ba:

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41: em_hg_inv:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	293	88.8	333	6	E30643
2	293	88.8	363	10	MUSL202IGK
3	293	88.8	714	6	BD090542
4	293	88.8	714	6	BD090651
5	293	88.8	714	6	E40005
6	293	88.8	714	6	E40813
7	293	88.8	714	6	E43359
8	293	88.8	877	6	E31225
9	293	88.8	925	6	E30616
10	293	88.8	925	6	E30617
11	289.8	87.8	354	10	MUSL711IGKV
12	289.8	87.8	363	10	MUSL931IGKV
13	289.8	87.8	393	10	AF045518
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15	288.2	87.3	333	10	MMAC005355
16	288.2	87.3	363	10	MUSL341IGKV
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23	285	86.4	334	6	E02169
24	285	86.4	336	10	MMIGLC310
25	285	86.4	336	10	MMIGLC404
26	285	86.4	393	10	S50265
27	285	86.4	396	10	AF207705
28	285	86.4	744	12	AF402256
29	283.6	85.9	333	10	AY173024
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37	277.6	84.1	351	10	MUSIGKABH
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ALIGNMENTS

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E30643

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

E30643
Antibody and nucleic acid encoding the same.
333 bp
DNA
linear
PAT 18-JUN-2001

E30643.1 GI:13017209

JP 1999332563-A/30.

Mus sp.

Mus sp.

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 333)

Mitsuharu, O., Takayuki, K. and Ixuo, M.

Antibody and nucleic acid encoding the same

Patent: JP 1999332563-A 30 07-DEC-1999;

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COMMENT
  ASahi CHEM IND CO LTD
  OS Mus sp. (mouse)
  PN JP 199332563-A/30
  PD 07-DEC-1999
  PR 26-MAY-1998 JP 1998163034
  PR MITSU HARU ONO, TAKAYUKI KUSAKA, IKUO MORIMOTO
  PI C12N15/02, A61K39/395, A61K39/395, C07K16/28, C12N15/09, C12P21/08,
  PC C12N15/00
  PC C12N15/00
  CC Strandedness: Double;
  CC Topology: Linear;
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RESULT 2
MUSL202IGK
LOCUS
DEFINITION
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ACCESSION
  M97869
VERSION
  M97869.1 GI:198867
KEYWORDS
  V-region; immunoglobulin light chain; immunoglobulin-kappa;
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SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 363)
  Lohman,K.L., Buck,D.W., Carrillo,M.A. and Kennedy,R.C.
  Characterization of murine monoclonal anti-CD4; epitope
  recognition, idiotype expression, and variable gene sequence
  Unpublished (1992)
  Original source text: Mus musculus (strain BALB/c, sub_species
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  Location/Qualifiers

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  Best Local Similarity 94.6%; Pred. No. 1.1e-88;
  Matches 315; Conservative 0; Mismatches 15; Indels 3; Gaps 1;

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RESULT 3
BD090542
LOCUS
DEFINITION
  Drug containing humanized anti-Fas antibody.
ACCESSION
  BD090542
VERSION
  BD090542.1 GI:22636152
KEYWORDS
  JP 2001342148-A/2.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  Serizawa,N., Haryuyama,H., Nakahara,K. and Tamaki,I.
  Drug containing humanized anti-Fas antibody
  Patent: JP 2001342148-A 2 11-DEC-2001;
  SANKYO CO LTD
  OS Mus musculus (mouse)
  EN JP 2001342148-A/2
  PD 11-DEC-2001
  PF 28-MAR-2001 JP 2001093106
  PI NOBUFUSA SERIZAWA,HIDEYUKI HARUYAMA,KAORI NAKAHARA,IKUKO PI
  TAMAKI
  PC A61K39/395,A61K38/00,A61P1/16,A61P7/06,A61P9/00,A61P9/10, PC
  A61P13/12,
  PC A61P19/02,A61P29/00,A61P37/00,A61P37/05,A61P37/08,A61P43/00//
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Ft mat_peptide (61) . (714)
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Best Local Similarity 94.6%; Pred. No. 1.2e-88;
Matches 315; Conservative 0; Mismatches 15; Indels 3; Gaps 1;

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Db 61 GACATTGCTCAGCCCAATCTCCAGCTCTTTGGCTGTGCTCTAGGGCAGAGGGCCACC 120
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RESULT 8

E31225
LOCUS
DEFINITION Device for separating CD4-positive cells and separation method.
ACCESSION E31225
VERSION E31225.1 GI:13017318
KEYWORDS JP 1999332594-A/3.
SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE E31225 877 bp DNA linear PAT 02-SEP-2002
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Mitsuhashi, O., Takayuki, K. and Ikuo, M.
TITLE Device for separating CD4-positive cells and separation method
JOURNAL Patent: JP 1999332594-A 3 07-DEC-1999;
ASAHI CHEM IND CO LTD

COMMENT

OS Mus sp. (mouse)
PN JP 1999332594-A/3
PD 07-DEC-1999
PF 26-MAY-1998 JP 1998163023
PR MITSUHASHI ONO, TAKAYUKI KUSAKA, IKUO MORIMOTO
PC C1201/04, C07K16/28, C07K16/46, C12M1/34, G01N33/53 CC
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FEATURES

source

BASE COUNT

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Query Match 88.8%; Score 293; DB 6; Length 877;
Best Local Similarity 94.6%; Pred. No. 1.2e-88;
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QY 178 GGGATCCAGCCAGCTTTAGTGGCAGTGGTCTGGACAGACTTCACCTCAACATCCAT 237
Db 199 GGGATCCAGCCAGCTTTAGTGGCAGTGGTCTGGACAGACTTCACCTCAACATCCAT 258
QY 238 CTGTGAGGAGGAGGATGCTGCAACCTATTACTGTGCTGAGCAAGTAAATGAGGATCTCTCC 297
Db 259 CTGTGAGGAGGAGGATGCTGCAACCTATTACTGTGCTGAGCAAGTAAATGAGGATCTCTCC 318
QY 298 AGCTTCGGTCTGGGACCAAGCTGGAGCTGAAA 330
Db 319 AGCTTCGGTGGAGGACCAAGCTGGAATCAAA 351

RESULT 9

E30616
LOCUS
DEFINITION Antibody and nucleic acid encoding the same.
ACCESSION E30616
VERSION E30616.1 GI:13017182
KEYWORDS JP 1999332563-A/3.
SOURCE Mus sp.
ORGANISM Mus sp.

REFERENCE

E30616 925 bp DNA linear PAT 18-JUN-2001
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Mitsuhashi, O., Takayuki, K. and Ikuo, M.
TITLE Antibody and nucleic acid encoding the same
JOURNAL Patent: JP 1999332563-A 3 07-DEC-1999;
ASAHI CHEM IND CO LTD
COMMENT OS Mus sp. (mouse)
PN JP 1999332563-A/3
PD 07-DEC-1999
PF 26-MAY-1998 JP 1998163034
PR MITSUHASHI ONO, TAKAYUKI KUSAKA, IKUO MORIMOTO
PC C12N15/02, A61K39/395, A61K39/395, C07K16/28, C12N15/09, C12P21/08,
PC C12N15/00,
PC C12N15/00,
CC Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..925
Location/Qualifiers
1..925
/organism="Mus sp."
/mol_type="genomic DNA"
/db_xref="taxon:10095"

FEATURES

source

BASE COUNT

ORIGIN

Query Match 88.8%; Score 293; DB 6; Length 925;
Best Local Similarity 94.6%; Pred. No. 1.2e-88;
Matches 315; Conservative 0; Mismatches 15; Indels 3; Gaps 1;

QY 1 GACATTGCTCACCACAAATCTCCAGCTCTTTGGCTGTGCTCTAGGGCAGAGGGCCACC 60
Db 67 GACATTGCTCAGCCCAATCTCCAGCTCTTTGGCTGTGCTCTAGGGCAGAGGGCCACC 126
QY 61 ATCTCTGCAAGCCAGCCAGCCAAAGTGTGATTATGATGGTGNAGTTATATG---TGGTAC 117
Db 127 ATCTCTGCAAGCCAGCCAGCCAAAGTGTGATTATGATGGTGNAGTTATATGAACTGGTAC 186
QY 118 CAACAGAAACACAGGACAGCCACCCAAATCTCTACCTATGCTGCAATCCAACTTAGAATCT 177
Db 187 CAACAGAAACACAGGACAGCCACCCAAATCTCTATGCTGCAATCCAACTTAGAATCT 246

QY 238 CCTGTGGAGGAGGATGCTGCAACCTATTACTGTACGCTTTGTAATGAGGATCCTCCC 297
 Db |||||
 QY 241 CCTGTGGAGGAGGAGGATGCTGCAACCTATTACTGTACGCTTTGTAATGAGGATCCTCCC 300
 Db |||||

QY 298 ACGTTTCGGTCTGGGACCAAGCTGGAGCTGAAA 330
 Db |||||

QY 301 ACGTTTCGGTCTGGGACCAAGCTGGAGCTGAAA 333
 Db |||||

Search completed: January 14, 2004, 17:00:19
 Job time : 1625.9 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 14, 2004, 14:23:59 ; Search time 169.524 Seconds
(without alignments)
5254.805 Million cell updates/sec

Title: US-09-759-112a-22

Perfect score: 330

Sequence: 1 gacattgtctaccacatcc.....ggaccaagctggagctgaaa 330

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	330	100.0	330	24	Murine Mab 1F7 lig
2	330	100.0	330	24	Murine Mab 1F7 lig
3	294.6	89.3	396	16	Mouse Mab 3B9 lig
4	294.6	89.3	396	20	Light chain variab
5	294.6	89.3	396	20	Light chain coding
6	293	88.8	333	21	Antibody 4H5 L cha
7	293	88.8	333	21	Murine derived DNA
8	293	88.8	714	19	Anti-Fas Mab HFE7A

9	293	88.8	714	21	AAA72109	cDNA encoding mous
10	293	88.8	714	21	AAA11547	Murine anti-Fas an
11	293	88.8	714	24	ABL45926	Mouse humanised an
12	293	88.8	714	24	ABL48669	Humanised anti-Fas
13	293	88.8	925	21	AZS58663	Antibody 4H5 H cha
14	293	88.8	925	21	AZS58664	Antibody 4H5 L cha
15	293	88.8	925	21	AZ44205	Murine derived DNA
16	293	88.8	925	21	AZ44206	Murine derived DNA
17	288.2	87.3	333	15	AAQ5554	Mouse anti-HIV mab
18	288.2	87.3	333	15	AAQ70372	Anti HIV antibody
19	286.6	86.8	333	24	ABK88124	DNA encoding mouse
20	286.6	86.8	831	24	AAZ29309	Human penton base
21	286.6	86.8	831	25	ABX12745	DNA encoding mouse
22	285	86.4	333	10	AAQ90492	Gene fragment of i
23	285	86.4	333	14	AAQ35609	Anti-CD4 antibody
24	285	86.4	733	13	AAQ25658	Mouse 0.5beta anti
25	285	86.4	780	10	AAQ90495	A v chi region gen
26	282.4	85.6	669	18	AAZ59338	MH1 monoclonal ant
27	280.8	85.1	900	11	AAQ04039	Anti-Leu 3a light
28	277	83.9	336	22	AAZ62145	Anti-SAF-1 monoclo
29	275.4	83.5	768	19	AAV70076	Anti-Fas humanised
30	275.4	83.5	768	21	AAZ72125	DNA encoding human
31	275.4	83.5	768	21	AAA11564	Humanised anti-Fas
32	275.4	83.5	768	24	ABL45943	Humanised anti-Fas
33	275.4	83.5	768	24	ABL48686	Humanised anti-Fas
34	273.8	83.0	309	21	AAZ58662	Antibody 4H5 L cha
35	273.8	83.0	309	21	AAZ44204	Murine derived DNA
36	272.2	82.5	768	19	AAV70075	Anti-Fas humanised
37	272.2	82.5	768	19	AAV70078	Anti-Fas humanised
38	272.2	82.5	768	21	AAZ72125	DNA encoding human
39	272.2	82.5	768	21	AAZ72177	DNA encoding human
40	272.2	82.5	768	21	AAA11563	Humanised anti-Fas
41	272.2	82.5	768	21	AAA11615	Humanised HFE7A de
42	272.2	82.5	768	24	ABL45942	Humanised anti-Fas
43	272.2	82.5	768	24	ABL45994	Humanised anti-Fas
44	272.2	82.5	768	24	ABL48685	Humanised anti-Fas
45	272.2	82.5	768	24	ABL48737	Humanised anti-Fas

ALIGNMENTS

RESULT 1
AAL48660
ID AAL48660 standard; DNA; 330 BP.
AC AAL48660;
XX
XX
XX 11-OCT-2002 (first entry)
XX Murine Mab 1F7 light chain coding sequence.
XX
XX Mouse; 1F7; antibody; immune modulator; anti-HIV antibody; CDR;
XX Complementarity determining region; framework-determining region;
XX FR; heavy chain; light chain; HIV infection; gene; ss.
XX Mus sp.
XX OS
XX WO200255668-A2.
XX
XX PD 18-JUL-2002.
XX
XX PF 11-JAN-2002; 2002WO-US00927.
XX
XX PR 11-JAN-2001; 2001US-0759112.
XX (IMMP-) IMMOPHERON INC.
XX
XX PI Muller S, Kohler H;
XX
XX DR WPI; 2002-590668/63.
XX
XX PT New polynucleotide encoding a complementarity- or framework-determining

PT region of an anti-idiotypic antibody that binds to human or primate
PT anti- human immunodeficiency virus (HIV) antibodies, for use in
XX vaccines against HIV
XX
PS Claim 10; Page 22-23; 27pp; English.
XX
CC The present invention relates to coding sequences of the murine 1F7
CC anti-idiotypic antibody complementarity-determining region (CDR) or
CC framework-determining region (FR). The antibody binds to human or primate
CC anti-human immunodeficiency virus (HIV) antibodies and can be used in the
CC treatment of HIV infection. The present sequence is the 1F7 light chain
XX coding sequence.
XX
SQ Sequence 330 BP; 80 A; 87 C; 83 G; 80 T; 0 other;
Query Match 100.0%; Score 330; DB 24; Length 330;
Best Local Similarity 100.0%; Pred. No. 2.1e-92;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GACATTGTGCTACCAATCTCCAGCTTCTTTGGCTGTCTCTAGGGCAGAGGCCACC 60
DB 1 GACATTGTGCTACCAATCTCCAGCTTCTTTGGCTGTCTCTAGGGCAGAGGCCACC 60
QY 61 ATCTCTGCAAGCCAGCCAAAGTGTGATTGATGCTGATAGTTATATGTGTACCAA 120
DB 61 ATCTCTGCAAGCCAGCCAAAGTGTGATTGATGCTGATAGTTATATGTGTACCAA 120
QY 121 CAGAAACACGAGCAGCCACCACCAACTCTCATCTGTCATCCCAATCTAGAACTGGG 180
DB 121 CAGAAACACGAGCAGCCACCACCAACTCTCATCTGTCATCCCAATCTAGAACTGGG 180
QY 181 ATCCAGCCAGGTTAGTGGCAGTGGTCTGGGACAGACTTCACCTCAACATCCATCT 240
DB 181 ATCCAGCCAGGTTAGTGGCAGTGGTCTGGGACAGACTTCACCTCAACATCCATCT 240
QY 241 GTGAGGAGGAGGATGCTGCAACTTACTGTGACGTTTGTAAATGAGGATCTCCACG 300
DB 241 GTGAGGAGGAGGATGCTGCAACTTACTGTGACGTTTGTAAATGAGGATCTCCACG 300
QY 301 TTGGTGTCTGGGACCAAGCTGGAGCTGAAA 330
DB 301 TTGGTGTCTGGGACCAAGCTGGAGCTGAAA 330
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ID AAL48661 standard; DNA; 330 BP.
XX
AC AAL48661;
XX
XX 11-OCT-2002 (first entry)
XX
XX Murine Mab 1F7 light chain coding sequence.
XX
XX
XX Mouse; 1F7; antibody; immune modulator; anti-HIV antibody; CDR;
XX complementarity determining region; framework-determining region;
XX FR; heavy chain; light chain; HIV infection; gene; ss.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
XX CDS 1..330
XX
XX /tag= a
XX /product= "1F7 light chain"
XX /partial
XX /note= "no start or stop codon"
XX
XX WO200255668-A2.
XX
XX 18-JUL-2002.
XX
XX 11-JAN-2002; 2002WO-US00927.
XX
XX

PR 11-JAN-2001; 2001US-0759112.
XX (IMMP-) IMMOPHERON INC.
XX
XX Muller S, Kohler H;
XX
XX WPI; 2002-590668/63.
XX P-PSDB; AAO18536.
XX
XX New polynucleotide encoding a complementarity- or framework-determining
XX region of an anti-idiotypic antibody that binds to human or primate
XX anti- human immunodeficiency virus (HIV) antibodies, for use in
XX vaccines against HIV
XX
PS Disclosure; Page 23; 27pp; English.
XX
CC The present invention relates to coding sequences of the murine 1F7
XX anti-idiotypic antibody complementarity-determining region (CDR) or
XX framework-determining region (FR). The antibody binds to human or primate
XX anti-human immunodeficiency virus (HIV) antibodies and can be used in the
XX treatment of HIV infection. The present sequence is the 1F7 light chain
XX coding sequence.
XX
SQ Sequence 330 BP; 80 A; 87 C; 83 G; 80 T; 0 other;
Query Match 100.0%; Score 330; DB 24; Length 330;
Best Local Similarity 100.0%; Pred. No. 2.1e-92;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GACATTGTGCTACCAATCTCCAGCTTCTTTGGCTGTCTCTAGGGCAGAGGCCACC 60
DB 1 GACATTGTGCTACCAATCTCCAGCTTCTTTGGCTGTCTCTAGGGCAGAGGCCACC 60
QY 61 ATCTCTGCAAGCCAGCCAAAGTGTGATTGATGCTGATAGTTATATGTGTACCAA 120
DB 61 ATCTCTGCAAGCCAGCCAAAGTGTGATTGATGCTGATAGTTATATGTGTACCAA 120
QY 121 CAGAAACACGAGCAGCCACCACCAACTCTCATCTGTCATCCCAATCTAGAACTGGG 180
DB 121 CAGAAACACGAGCAGCCACCACCAACTCTCATCTGTCATCCCAATCTAGAACTGGG 180
QY 181 ATCCAGCCAGGTTAGTGGCAGTGGTCTGGGACAGACTTCACCTCAACATCCATCT 240
DB 181 ATCCAGCCAGGTTAGTGGCAGTGGTCTGGGACAGACTTCACCTCAACATCCATCT 240
QY 241 GTGAGGAGGAGGATGCTGCAACTTACTGTGACGTTTGTAAATGAGGATCTCCACG 300
DB 241 GTGAGGAGGAGGATGCTGCAACTTACTGTGACGTTTGTAAATGAGGATCTCCACG 300
QY 301 TTGGTGTCTGGGACCAAGCTGGAGCTGAAA 330
DB 301 TTGGTGTCTGGGACCAAGCTGGAGCTGAAA 330
RESULT 3
AAQ83490
ID AAQ83490 standard; cDNA; 396 BP.
XX
XX AAQ83490;
XX
XX 25-MAR-2003 (updated)
XX 20-SEP-1995 (first entry)
XX
XX Mouse Mab 3B9 light chain.
XX
XX Chimeric antibody; humanized antibody; antibody engineering;
XX monoclonal antibody; Mab; interleukin-4; IL-4; allergy; ds.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
XX CDS 1..396
XX
XX /*tag= a
XX

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FT sig_peptide 1..60
FT mat_peptide /*tag= b
FT 61..396
FT /*tag= c
XX
XX WO9507301-A1.
XX 16-MAR-1995.
XX
XX 07-SEP-1994; 94WO-US10308.
XX
XX 07-SEP-1993; 93US-0117366.
XX 14-OCT-1993; 93US-0136783.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Gross MS, Holmes SD, Sylvester DR;
XX
XX WPI; 1995-123387/16.
XX P-PSDB; AAR70189.
XX
XX Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
XX from high affinity mAbs - useful in treatment of IL-4-mediated
XX PT and IgE-mediated allergic conditions
XX
XX Disclosure; Fig.1; 97pp; English.
XX
XX Spleen cells from mice immunized with human IL-4 were used to prepare
XX hybridomas, which were screened for anti-IL-4 Mab secretion. Only
XX clone 3B9 was positive. cDNA clones of the 3B9 light and heavy
XX chains were cloned into pGEM7f+ and transformed into E. coli
XX DH5-alpha. The clones were sequenced (AAQ83490-91), and used for
XX antibody engineering.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 396 BP; 99 A; 103 C; 103 G; 91 T; 0 other;
XX
XX Query Match 89.3%; Score 294.6; DB 16; Length 396;
XX Best Local Similarity 94.9%; Pred. No. 2.2e-81;
XX Matches 316; Conservative 0; Mismatches 14; Indels 3; Gaps 1;
XX
XX 1 GACATTGTGCTCACCATTCTCCAGTCTCTTGGCTGTGCTCTAGGGCAGAGGGCCACC 60
XX 61 GACATTGTGCTGACCCAACTCCAGCTTCTTGGCTGTGCTCTAGGGCAGAGGGCCACC 120
XX 61 ATCTCTGCAAGCCAGCCAAAGTGTGATGATGGTGATAGTTATATG---TGGTAC 117
XX 121 ATCTCTGCAAGCCAGCCAAAGTGTGATGATGGTGATAGTTATATGAACTGGTAC 180
XX 118 CAACAGAAACCCAGGAGGAGGATGCTGCAACCTTATCTGTGCAAGGATCTCCG 237
XX 181 CAACAGAAACCCAGGAGGAGGATGCTGCAACCTTATCTGTGCAAGGATCTCCG 240
XX 178 GGGATCCCGAGGAGGATGCTGCAACCTTATCTGTGCAAGGATCTCCG 237
XX 241 GGGATCCCGAGGAGGATGCTGCAACCTTATCTGTGCAAGGATCTCCG 300
XX 238 CCTGTGGAGGAGGATGCTGCAACCTTATCTGTGCAAGGATCTCCG 297
XX 301 CCTGTGGAGGAGGATGCTGCAACCTTATCTGTGCAAGGATCTCCG 360
XX 298 ACCTTCGGTGTGGGACCAAGCTGGAGCTGAAA 330
XX 361 ACCTTCGGTGTGGGACCAAGCTGGAGCTGAAA 393
XX
XX RESULT 4
XX AAX85884
XX ID AAX85884 standard; cDNA; 396 BP.
XX
XX AAX85884;
XX

```

```

DT 13-SEP-1999 (first entry)
XX
XX Light chain variable region cDNA of murine IL-4 antibody 3B9.
XX
XX Light chain variable region; interleukin-4; IL-4; antibody 3B9;
XX chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;
XX immunoglobulin E-mediated allergic reaction; allergic rhinitis;
XX conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
XX rheumatoid arthritis; host-versus-graft disease; renal disease;
XX allergy; ds.
XX
XX Mus sp.
XX
XX US5928904-A.
XX
XX 27-JUL-1999.
XX
XX 07-JUN-1995; 95US-0483632.
XX
XX 07-JUN-1995; 95US-0483632.
XX 14-OCT-1993; 93US-0117366.
XX 14-OCT-1993; 93US-0136783.
XX 07-SEP-1994; 94WO-US10308.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Gross MS, Holmes SD, Sylvester DR;
XX
XX WPI; 1999-429500/36.
XX P-PSDB; AAY23767.
XX
XX New DNA molecules encoding recombinant antibodies useful for
XX treating IL4-mediated conditions
XX
XX Example 3; Fig 1; 50pp; English.
XX
XX The present sequence encodes the light chain variable region of
XX murine interleukin-4 (IL-4) antibody 3B9. The sequences are used
XX in the production of chimeric and humanised IL-4 monoclonal antibodies.
XX The antibodies of the invention are used in therapeutic and
XX immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis,
XX conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock,
XX rheumatoid arthritis, host-versus-graft disease and renal disease.
XX They are also useful in the diagnosis of an allergy or condition
XX associated with excess IL-4 production through the measurement e.g. by
XX ELISA of circulating endogenous IL-4 levels in humans.
XX
XX Sequence 396 BP; 99 A; 103 C; 103 G; 91 T; 0 other;
XX
XX Query Match 89.3%; Score 294.6; DB 20; Length 396;
XX Best Local Similarity 94.9%; Pred. No. 2.2e-81;
XX Matches 316; Conservative 0; Mismatches 14; Indels 3; Gaps 1;
XX
XX 1 GACATTGTGCTCACCATTCTCCAGTCTCTTGGCTGTGCTCTAGGGCAGAGGGCCACC 60
XX 61 GACATTGTGCTGACCCAACTCCAGCTTCTTGGCTGTGCTCTAGGGCAGAGGGCCACC 120
XX 61 ATCTCTGCAAGCCAGCCAAAGTGTGATGATGGTGATAGTTATATG---TGGTAC 117
XX 121 ATCTCTGCAAGCCAGCCAAAGTGTGATGATGGTGATAGTTATATGAACTGGTAC 180
XX 118 CAACAGAAACCCAGGAGGAGGATGCTGCAACCTTATCTGTGCAAGGATCTCCG 177
XX 181 CAACAGAAACCCAGGAGGAGGATGCTGCAACCTTATCTGTGCAAGGATCTCCG 240
XX 178 GGGATCCCGAGGAGGATGCTGCAACCTTATCTGTGCAAGGATCTCCG 237
XX 241 GGGATCCCGAGGAGGATGCTGCAACCTTATCTGTGCAAGGATCTCCG 300
XX 238 CCTGTGGAGGAGGATGCTGCAACCTTATCTGTGCAAGGATCTCCG 297
XX

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QY 238 CCTGTGGAGGAGAGATCTCCACCTATTACTCTCAGCTTTGTAATGAGATCCTCCC 297
 Db 241 CCTGTGGAGGAGAGATCTCCACCTATTACTCTCAGCTTTGTAATGAGATCCTCCG 300

QY 298 ACCTTCGGTCTGGGACCAAGCTGGAGCTGAAA 330
 Db 301 ACCTTCGGTGGAGGACCAAGCTGGAGTCAAA 333

RESULT 7
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 ID AAZ44232 standard; DNA; 333 BP.
 XX
 AC AAZ44232;
 XX
 DT 31-MAR-2000 (first entry)
 XX
 DE Murine derived DNA fragment #6.
 XX
 KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
 KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
 KW HIV infection; autoimmune disease; murine; ds.
 XX
 OS Mus sp.
 XX
 PN WO9961629-A1.
 XX
 PD 02-DEC-1999.
 XX
 PP 24-MAY-1999; 99WO-JP02711.
 XX
 PR 25-MAY-1998; 98JP-0159957.
 PR 26-MAY-1998; 98JP-0163023.
 XX
 PA (ASAH) ASARI KASEI KOGYO KK.
 PA (ASAH) ASARI MEDICAL CO LTD.
 XX
 PI Ono M, Soka T, Morimoto I, Miyamura K;
 XX
 DR WPI; 2000-086720/07.
 DR P-PSDB; AAY51146.
 XX
 PT Devices containing antibodies recognising CD4 or CD34 and their use for
 PT the separation of CD4 or CD34 positive cells -
 XX
 PS Disclosure; Page 97-98; 11pp; Japanese.
 XX
 CC This invention describes a novel device (I) for separating cluster
 CC differentiation (CD)-positive cells using a recombinant (chimeric or
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful
 CC for the separation of CD4 or CD34 positive cells, which is useful for
 CC the collection of hematopoietic undifferentiated cells, elimination of
 CC lymphocytes from cells to be used in bone marrow transplantation, the
 CC detection of leukemic cells and the production of medicinal
 CC compositions for the treatment of HIV infection and autoimmune diseases.
 CC This sequence encodes a murine derived protein fragment which is used
 CC to illustrate the method of the invention.
 XX
 SQ Sequence 333 BP; 87 A; 86 C; 84 G; 76 T; 0 other;

Query Match 88.8%; Score 293; DB 21; Length 333;
 Best Local Similarity 94.6%; Pred. No. 6.6e-81;
 Matches 315; Conservative 0; Mismatches 15; Indels 3; Gaps 1;

QY 1 GACATTGTGCTCACCAATCTCCAGTTCTTTGGTGTCTCTTAGGGCAGAGGCCACC 60
 Db 1 GACATTGTGCTGACCAATCTCCAGTTCTTTGGTGTCTCTTAGGGCAGAGGCCACC 60
 QY 61 ATCTCTGCAAGGCCAGCCAAAGTGTGATTATGATGGTATAGTTATATG---TGSTAC 117
 Db 61 ATCTCTGCAAGGCCAGCCAAAGTGTGATTATGATGGTATAGTTATGAACTGGGTAC 120

QY 118 CAACAGAAACAGGACAGCCACCAACTCTCTCAGCTATCTGATCCATCTAGAAATCT 177
 Db 121 CAACAGAAACAGGACAGCCACCAACTCTCTCATCTATCTGCATCCAAATCTAGAATCT 180
 QY 178 GGGATCCAGCCAGGTTTGTAGTGGCAGTGGTCTGGGACAGACTTCCACCTCAACATCCAT 237
 Db 181 GGGATCCAGCCAGGTTTGTAGTGGCAGTGGTCTGGGACAGACTTCCACCTCAACATCCAT 240
 QY 238 CCTGTGGAGGAGGAGTCTGCAACTATTACTGTGAGCTTTGTAATGAGGATCCTCCC 297
 Db 241 CCTGTGGAGGAGGAGTCTGCAACTATTACTGTGAGGATAGTGGATCCTCCG 300

QY 298 ACCTTCGGTCTGGGACCAAGCTGGAGCTGAAA 330
 Db 301 ACCTTCGGTGGAGGACCAAGCTGGAGTCAAA 333

RESULT 8
 AAV70130
 ID AAV70130 standard; cDNA to mRNA; 714 BP.
 XX
 AC AAV70130;
 XX
 DT 25-MAR-2003 (updated)
 DT 15-MAR-1999 (first entry)
 XX
 DE Anti-Fas MAb HPE7A light chain cDNA.
 XX
 KW HPE7A; monoclonal antibody; mouse; Fas; humanised antibody;
 KW apoptosis; HPE7A; autoimmune disease; Hashimoto's disease;
 KW systemic lupus erythematosus; graft versus host disease;
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 KW transplant rejection; therapy; ds.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT sig_peptide i..60 /*tag= a
 FT mat_peptide 61..714 /*tag= b
 FT
 XX
 XX AU9859701-A.
 XX
 PD 08-OCT-1998.
 XX
 PP 30-MAR-1998; 98AU-0059701.
 XX
 PR 08-OCT-1997; 97JP-0276064.
 PR 01-APR-1997; 97JP-0082953.
 PR 25-JUN-1997; 97JP-0169088.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 PI Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
 XX
 DR WPI; 1998-543440/01.
 DR P-PSDB; AAW83042.
 XX
 PT New antibodies and proteins bind conserved epitope of Fas antigen -
 PT used to evaluate drugs in animal models and to treat Fas-associated
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 PT myocarditis, hepatitis and AIDS
 XX
 PS Reference Example 4; Page 188-189; 292pp; English.
 XX

KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus; HFE7A;
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection; ss.
OS Mus musculus.
XX
XX EP990663-A2.
XX
XX 05-APR-2000.
XX 29-SEP-1999; 99EP-0307711.
XX
XX 30-SEP-1998; 98JP-0276881.
PR 30-SEP-1998; 98JP-0276882.
XX
XX (SANY) SANKYO CO LTD.
XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
XX WPI; 2000-258930/23.
DR P-PSDB; AAW90898.
XX
XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
PT inflammatory or autoimmune disease, induces apoptosis selectively in
PT cells with abnormal Fas-Fas ligand systems -
XX
XX Example reference 4; Page 102-103; 263pp; English.
XX
XX This invention describes a novel humanized anti-Fas antibody-like
CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
CC ligand system, by binding to Fas on the cell surface, and prevents
CC apoptosis in cells with a normal system, by inhibiting binding between
CC Fas and its ligand. The products of the invention have anti-inflammatory,
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
CC apoptosis by binding to cell surface Fas or inhibit it by competitive
CC inhibition of ligand binding. (I) are used to treat and/or prevent
CC diseases associated with the Fas/Fas ligand system, especially systemic
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
CC inhibit apoptosis in normal cells but selectively induce it in abnormal
CC cells. They bind to both human and murine Fas, so can be evaluated in
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
CC the native ligand, do not induce liver disease, and have reduced risk of
CC inducing a human anti-murine antibody response. This sequence encodes
CC a murine anti-Fas monoclonal antibody HFE7A light chain described in the
XX method of the invention.
XX
SQ Sequence 714 BP; 200 A; 184 C; 173 G; 157 T; 0 other;
Query Match 88.8%; Score 293; DB 21; Length 714;
Best Local Similarity 94.6%; Pred. No. 8.5e-81;
Matches 315; Conservative 0; Mismatches 15; Indels 3; Gaps 1;
QY 1 GACATTGCTCACCACAAATCTCCAGCTCTTTGGCTGTCTCTAGGGCAGAGGCCACC 60
DB 61 GACATTGCTCAGCCAAATCTCCAGCTCTTTGGCTGTCTCTAGGGCAGAGGCCACC 120

QY 61 ATCTCTGCAAGGCCAGCCAAAGTGTGATTATGATGCTGATGTTATATG---TGGTAC 117
DB 121 ATCTCTGCAAGGCCAGCCAAAGTGTGATTATGATGCTGATGTTATATGAACTGGTAC 180
QY 118 CAACAGAAACCCAGGACAGCCACCAAACTCCTCACTATCTCTGTCATCCCAATCTAGAATCT 177
DB 181 CAACAGAAACCCAGGACAGCCACCAAACTCCTCATCTATCTGTCATCCCAATCTAGAATCT 240
QY 178 GGGATCCCGCCAGGTTTGTAGTGGCAGTGGCTCTGGGACAGACTTCACCCCTCAACATCCAT 237
DB 241 GGGATCCCGCCAGGTTTGTAGTGGCAGTGGCTCTGGGACAGACTTCACCCCTCAACATCCAT 300
QY 238 CCTGTGGAGGAGGAGGATGCTCAACCTATTACTGTGCTGAGCTTTGTATGAGGATCCTCCC 297
DB 301 CCTGTGGAGGAGGAGGATGCTCAACCTATTACTGTGCTGAGGATGAGGATCCTCCG 360
QY 298 ACCTTCGGTCTGGGACCAAGCTGGAGCTGAAA 330
DB 361 ACCTTCGGTGGAGGACCAAGCTGGAAATCAA 393
RESULT 11
ABL45926
ID ABL45926 standard; cDNA; 714 BP.
XX
XX ABL45926;
AC
XX
DT 26-APR-2002 (first entry)
XX
XX Mouse humanised anti-Fas antibody related cDNA SEQ ID NO 8.
DE Human; mouse; humanised anti-Fas antibody; Fas/Fas ligand;
KW light chain subunit; apoptosis; immunosuppressive; antiallergic;
KW autoimmune disease; allergy; atopic; ss.
XX
XX Mus musculus.
OS
XX
XX JP2001342148-A.
XX
PD 11-DEC-2001.
XX
XX 28-MAR-2001; 2001JP-0093106.
XX
XX 29-MAR-2000; 2000JP-0090918.
PR
XX (SANY) SANKYO CO LTD.
XX
XX WPI; 2002-145113/19.
DR
XX P-PSDB; ABB74904.
XX
XX Drug containing humanised anti-Fas antibody, used for preventing and
PT treating autoimmune diseases, allergy, and atopy -
XX
XX Example 4 (Preparatory); Page 77-79; 194pp; Japanese.
XX
XX The invention relates to a preventive or treating agent for diseases
CC caused by abnormality in Fas/Fas ligand system containing as the active
CC component an antibody having as the light chain subunit a polypeptide
CC containing residues 1-218 of one of 3, 239 residue amino acid sequences,
CC or residues 1-451 of one of 3, 470 residue amino acid sequences, all
CC fully defined in the specification and having an activity of combining
CC specifically with mammalian Fas and an activity of inducing apoptosis
CC in a cell expressing Fas. The agent has immunosuppressive and
CC antiallergic activity and is used for preventing and treating autoimmune
CC diseases, allergy, atopy and others.
XX
SQ Sequence 714 BP; 200 A; 184 C; 173 G; 157 T; 0 other;
Query Match 88.8%; Score 293; DB 24; Length 714;
Best Local Similarity 94.6%; Pred. No. 8.5e-81;
Matches 315; Conservative 0; Mismatches 15; Indels 3; Gaps 1;
QY 1 GACATTGCTCACCACAAATCTCCAGCTCTTTGGCTGTCTCTAGGGCAGAGGCCACC 60

Qy	61	ATCTCCTGCAGGCCAGCCAAAGTGTTCATTTATGATGGTGTATGTTATATG---TGGTAC	117
Db	127	ATCTCCTGCAGGCCAGCCAAAGTGTTCATTTATGATGGTGTATGTTATATGAACTGGTAC	186
Qy	118	CAACAGAAACCCAGGACAGCCACCCAAACTCCTCACCTTATGTCATCCAACTCTAGAATCT	177
Db	187	CAACAGAAACCCAGGACAGCCACCCAAACTCCTCATCTATGTCATCCAACTCTAGAATCT	246
Qy	178	GGGATCCCGCCAGGTTTATGTGGCAGTGGGTCTGGGACAGACTTCACCCCTCAACATCCAT	237
Db	247	GGGATCCCGCCAGGTTTATGTGGCAGTGGGTCTGGGACAGACTTCACCCCTCAACATCCAT	306
Qy	238	CCTGTGGAGGAGGAGGATGCTSCAACCTATTACTGTCTCAGCTTTGTAAATGAGGATCCTCCC	297
Db	307	CCTGTGGAGGAGGAGGATGCTSCAACCTATTACTGTCTCAGCAAAAGTAGTGAGGATCCTCCG	366
Qy	298	ACGTTCCGTGCTGGACCAAGCTGGAGCTGAAA	330
Db	367	ACGTTCCGTGAGGACCAAGCTGGAAATCAAA	399

Search completed: January 14, 2004, 16:03:13
 Job time : 171.524 secs

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 14, 2004, 15:52:50 / Search time 1328.1 Seconds
(without alignments)
6039.083 Million cell updates/sec

Title: US-09-759-112a-22
Perfect score: 330
Sequence: 1 gacattgctcaccattc.....ggaccagctggagctgaaa 330

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: em_estba.*

2: em_esthum.*

3: em_estin.*

4: em_estnu.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_htc.*

9: gb_est1.*

10: gb_est2.*

11: gb_htc.*

12: gb_est3.*

13: gb_est4.*

14: gb_est5.*

15: em_estfun.*

16: em_estom.*

17: em_gss_hum.*

18: em_gss_inv.*

19: em_gss_pln.*

20: em_gss_vrt.*

21: em_gss_fun.*

22: em_gss_mam.*

23: em_gss_mus.*

24: em_gss_pro.*

25: em_gss_rtd.*

26: em_gss_phg.*

27: em_gss_vrl.*

28: gb_gss1.*

29: gb_gss2.*

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	250.4	75.9	659	10	BF137298
2	249.8	75.7	407	10	AW988429
3	245	74.2	683	11	AF240172
4	245	74.2	1108	12	BG969221

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

5	244.8	74.2	774	10	BF581989
6	244	73.9	750	12	BG965050
7	241.8	73.3	398	9	AA423447
8	241.8	73.3	643	14	BY733441
9	240.4	72.8	831	12	BG966589
10	239.6	72.6	402	9	AI549800
11	239.2	72.5	377	10	BG148320
12	239.2	72.5	876	12	BI107286
13	238.6	72.3	735	12	BG967206
14	238.6	72.3	865	12	BI659552
15	238	72.1	420	9	AI120005
16	237.6	72.0	732	12	BG962768
17	235.4	71.3	806	12	BI108506
18	232.2	70.4	1063	10	BF577971
19	224.2	67.9	922	10	BF584560
20	216	65.5	974	10	BF577946
21	207	62.7	286	10	BG144775
22	201.6	61.1	339	9	AA710249
23	200.4	60.7	266	10	BG145361
24	199.4	60.4	344	13	BY214260
25	198.6	60.2	577	28	AZ942606
26	175.4	53.2	671	11	AF240168
27	174.2	52.8	268	10	BG148476
28	171.2	51.9	756	28	BH054133
29	169.8	51.5	757	10	BG484518
30	164.4	49.8	465	9	AW404697
31	164.4	49.8	727	14	CB956193
32	163.8	49.6	798	10	BG426036
33	162.2	49.2	776	14	CB959429
34	161.2	48.8	755	14	CB957520
35	160.6	48.7	533	9	AW802126
36	160.6	48.7	717	14	CB957784
37	160.6	48.7	777	14	CB957974
38	160.6	48.7	779	14	CB986877
39	160.6	48.7	795	14	CB986276
40	160.6	48.7	889	14	CB985667
41	160.4	48.6	434	9	AW406486
42	160.2	48.5	808	14	CB984840
43	159.6	48.4	482	9	AV733856
44	159.6	48.4	519	9	AW405183
45	159.6	48.4	744	14	CB956406

ALIGNMENTS

RESULT 1

BF137298

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BF137298 659 bp mRNA linear EST 24-OCT-2000
601781658F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4009670 5',
mRNA sequence.

BF137298.1 GI:10976338

EST.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;

NIH-MGC http://mgi.nci.nih.gov/

1 (bases 1 to 659)

NIH-MGC

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLM9246 row: c column: 15

High quality sequence stop: 657.

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

The WashU-HMI Mouse EST Project

Unpublished

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mousees@wustl.edu

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:492708

Seq primer: -28ml3 rev2 ET from Amersham.

Location/Qualifiers

1..398

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="IMAGE:832492"

/sex="male"

/tissue_type="mammary gland"

/dev_stage="4 weeks"

/lab_host="DH103"

/clone_lib="Soares mammary gland NBMWG"

/notes="Organ: mammary gland; Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5']

TGTTACCACTGAAGTGGAGCGCCGCCAGATGTTTTTTTTTTTTTTTTTTTTTTT

T 3'); double-stranded cDNA was ligated to Eco RI

adaptors (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of the modified p773 vector.

RNA provided by Dr. Minoru Ko, Wayne State Univ. Library

constructed and normalized by Bento Soares and M. Fatima

Bonaldo."

BASE COUNT 101 a 100 c 102 g 95 t

ORIGIN

Query Match 73.3%; Score 241.8; DB 9; Length 398;

Best Local Similarity 85.0%; Pred. No. 5.2e-61;

Matches 283; Conservative 0; Mismatches 47; Indels 3; Gaps 1;

QY 1 GACATTGTGCTACCAATTCACGCTTCTTTGGCTGTCTCTAGGGCAGAGGCCACC 60

DB 66 GACATTGTGCTGACCAATTCACGCTTCTTTGGCTGTCTCTAGGGCAGAGGCCACC 125

QY 61 ATCTCTGCGAGCCGACCCAGAGTGTGATTATGATGTTGATGATATG---TGGTAC 117

DB 126 ATCTCTGCGAGCCGACCCAGAGTGTGATTATGATGTTGATGATATG---TGGTAC 185

QY 118 CAACGAACACCGAGCAGCAGCCACCAACCTCCATCTGCTGCAATCCAACTAGAACT 177

DB 186 CAACGAACACCGAGCAGCAGCCACCAACCTCCATCTGCTGCAATCCAACTAGAACT 245

QY 178 GGGATCCGAGCCAGGTTTATGTCAGTGGTCTGGGACAGATTCACCTCCAACTCCAT 237

DB 246 GGGGTCCTCCGACGAGTTTATGTCAGTGGTCTGGGACAGATTCACCTCCAACTCCAT 305

QY 238 CTGTGGAGGAGGAGATGCTGCAACTATTACTGTGACCTTTGTAATGAGATCCTCC 297

DB 306 CCTATGAGGAGGAGATGATCACTATGTTTCTGTGACCAAGTAGAGATTCCTCGG 365

QY 298 AGTTCCGTCGTCGGGACCAAGCTGGAGCTGAAA 230

DB 366 AGTTCCGTCGTCGGGACCAAGCTGGAGCTGAAA 398

RESULT 8

BY733441

LOCUS

DEFINITION

BY733441

VERSION

KEYWORDS

SOURCE

ORGANISM

643 bp mRNA linear EST 17-DEC-2002

LYmph node Mus musculus cDNA clone G630004K22 5', mRNA sequence.

BY733441.1 GI:27146568

EST

Mus musculus (house mouse)

REFERENCE

AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 643)

Nikaido, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V., Chothia, C. F., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Petrea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, Z., Zavalan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hata, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, Z. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL

MEDLINE

PUBMED

12466851

Contact: Yoshihide Hayashizaki

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The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-resgsc.riken.go.jp

URL: http://genome.gsc.riken.go.jp/

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, P., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ono, M., Ohsato, N., Saito, R., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y., Waki, K., Watanabe, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.

FEATURES

Location/Qualifiers
source

1..643
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="G630004K22"
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accessory axillary lymph node"
168 a 165 c 156 g 151 t 3 others

BASE COUNT

168 a 165 c 156 g 151 t 3 others

ORIGIN

Query Match 73.3%; Score 241.8; DB 14; Length 643;
Best Local Similarity 85.0%; Pred. No. 6.9e-61;
Matches 283; Conservative 0; Mismatches 47; Indels 3; Gaps 1;
QY 1 GACATGTGCTCACCACCAATCTCCAGCTTCTTGGCTGTCTCTAGGCGCAGAGGCCACC 60
Db 91 GACATGTGCTCACCACCAATCTCCAGCTTCTTGGCTGTCTCTAGGCGCAGAGGCCACC 150
QY 61 ATCTCTCTCAAGGCGCAGCCAAAGTGTGATATGATGCTGATAGTTATAT---GTGGTAC 117
Db 151 ATCTCTCTCAGAGCGCAGCGAAGTGTGTAATATGTCATAGTTATTAACCTGGTTC 210
QY 118 CAACGAAACACGAGCAGCAGCCAACTCTCTCAGCTATGCTGCATCCAACTAGATCT 177
Db 211 CAACGAAACACGAGCAGCAGCCAACTCTCTCAGCTATGCTGCATCCAACTAGATCT 270
QY 178 GCGATCCACGAGCAGGTTAGTGGCAGTGGTCTGGGACAGACTTCACCCCTCAACATCCAT 237
Db 271 GGAGTCCCTGCCAGGTTAGTGGCAGTGGTCTGGGACAGACTTCACCCCTCAACATCCAT 330
QY 238 CTGTGGAGAGAGAGATGCTGCACCTATTAATCTCAGCTTTGTAATGAGATCCCTCC 297
Db 331 CCTATGGAGAGAGATGATCTCAGCTGATTTCTCTCAGCAAAAGTAAGAGAGTTCCGTGG 390
QY 298 ACGTTCCGCTGGGACCAAGCTGGAGCTGAAA 330
Db 391 ACGTTCCGCTGGGACCAAGCTGGAGCTGAAA 423

RESULT 9

BG966589
LOCUS 831 bp mRNA linear EST 12-JUN-2001
DEFINITION 602834422F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4989053 5',
mRNA sequence.
ACCESSION BG966589
VERSION BG966589.1 GI:14354226
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE

1 (bases 1 to 831)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>
Plate: LLML1002 row: k column: 06
High quality sequence stop: 801.
Location/Qualifiers

FEATURES

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/db_xref="taxon:10090"
/clone="IMAGE:4989053"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Co24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site: 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 230 a 219 c 197 g 185 t

ORIGIN

Query Match 72.8%; Score 240.4; DB 12; Length 831;
Best Local Similarity 86.5%; Pred. No. 2.1e-60;
Matches 289; Conservative 0; Mismatches 41; Indels 4; Gaps 2;
QY 1 GACATGTGCTCACCACCAATCTCCAGCTTCTTGGCTGTCTCTAGGCGCAGAGGCCACC 60
Db 74 GACATGTGCTCACCACCAATCTCCAGCTTCTTGGCTGTCTCTAGGCGCAGAGGCCACC 133
QY 61 ATCTCTCTCAAGGCGCAGCCAAAGTGTGATATGATGCTGATAGTTATATG---TGGTAC 117
Db 134 ATCTCTCTCAGAGCGCAGCGAAGTGTGTAATATGTCATAGTTATGAACCTGGTTC 193
QY 118 CAACGAAACACGAGCAGCAGCCAACTCTCAGCTATGCTGCATCCAACTAGATCT 177
Db 194 CAACGAAACACGAGCAGCAGCCAACTCTCAGCTATGCTGCATCCAACTAGATCT 253
QY 178 GCGATCCACGAGCAGGTTAGTGGCAGTGGTCTGGGACAGACTTCACCCCTCAACATCCAT 237
Db 254 GCGGTCCTGCCAGGTTAGTGGCAGTGGTCTGGGACAGACTTCAGCCCTCAACATCCAT 313
QY 238 CTGTGGAGAGAGAGATGCTGCACCTATTAATCTCAGCTTTGTAATGAGATCCCTCC 296
Db 314 CCTATGGAGAGAGATGATCTCAGCTGATTTCTCTCAGCAAAAGTAAGAGAGTTCCGTGG 373
QY 297 ACGTTCCGCTGGGACCAAGCTGGAGCTGAAA 330
Db 374 GACGTTCCGCTGGGACCAAGCTGGAGCTGAAA 407

RESULT 10

AI549800
LOCUS 402 bp mRNA linear EST 23-MAR-1999
DEFINITION ve80a03.Y1 Soares mammary_gland NM0MG Mus musculus cDNA clone
IMAGE:832492 5' similar to gb:M63438 IG KAPPA CHAIN PRECURSOR V-III
REGION (HUMAN); gb:M5669 Mouse Ig aberrantly rearranged
kappa-chain mRNA V-J2-C-region, (MOUSE);, mRNA sequence.
ACCESSION AI549800
VERSION AI549800.1 GI:4482163
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE

1 (bases 1 to 402)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
This clone is available royalty-free through LLML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:492708
This read is a RESEQUENCE of a previously sequenced mouse clone

This read has been verified (found to hit its original self in the correct orientation)

Seq primer: -4ORP from Gibco.

FEATURES

Location/Qualifiers
1..402
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CS7BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:832492"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_lib="Soares mammary gland NBMG"
/note="Organ: mammary gland; Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo (dT) primer [5, TGTACCAATCTGAAGTGGAGCGCGCGGATGTTTTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 102 a 101 c 105 g 94 t
ORIGIN

Query Match 72.6%; Score 239.6; DB 9; Length 402;
Best Local Similarity 85.6%; Pred. No. 2.4e-60;
Matches 279; Conservative 0; Mismatches 44; Indels 3; Gaps 1;
QY 1 GACATGTGCTCACCAGTCTCCAGCTCTTTGGCTGTCTTAGGGCAGAGGCCACC 60
Db 66 GACATGTGCTGACCAATCTCCAGCTCTTTGGCTGTCTTAGGGCAGAGGCCACC 125
QY 61 ATCTCTCTCAAGCCAGCCAGCAAGTGTGATGATGATGATGATGATGATGATG 117
Db 126 ATCTCTCTGAGCCAGGAGGAGTGTGATGATGATGATGATGATGATGATG 185
QY 118 CAACAGAAACAGGACAGCCACCCAACTCTCTACCTATGCTGATGATGATGATG 177
Db 186 CAACAGAAACAGGACAGCCACCCAACTCTCTACCTATGCTGATGATGATGATG 245
QY 178 GGGATCCAGCCAGGATTTAGTGGAGTGGTCTGGAGCAGACTTCACTCAATCAT 237
Db 246 GGGATCCAGGATTTAGTGGAGTGGTCTGGAGCAGACTTCACTCAATCAT 305
QY 238 CTTGTGGAGGAGGATGCTGCACTTATCTGCTGCTGCTGCTGCTGCTGCTGCTG 297
Db 306 CTTGTGGAGGAGGATGCTGCACTTATCTGCTGCTGCTGCTGCTGCTGCTGCTG 365
QY 298 ACGTTCGGTCTGGACCAAGCTGGA 323
Db 366 ACGTTCGGTGGAGCCACCAAGCTGGA 391

RESULT 11
Bg148320 327 bp mRNA linear EST 01-FEB-2001
LOCUS
DEFINITION
IMAGE:3383818 5', similar to SW:KV3H MOUSE P01660 IG KAPPA CHAIN V-III REGION PC 3741/TSFC 111. ; mRNA sequence.
ACCESSION
Bg148320
VERSION
Bg148320.1 GI:12651742
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 327)
AUTHORS
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgaps@mail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1088814
Seq primer: -4ORP from Gibco.

Location/Qualifiers
1..327
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:3383818"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Soares mouse NMGB bccll"
/note="Organ: germinal B-cell; Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo (dT) primer [5, TGTACCAATCTGAAGTGGAGCGCGCGGATGTTTTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. Library is normalized; constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 83 a 84 c 82 g 78 t
ORIGIN

Query Match 72.5%; Score 239.2; DB 10; Length 327;
Best Local Similarity 85.8%; Pred. No. 2.8e-60;
Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;
QY 10 CTCAACAACTCTCCAGCTCTTTGGCTGTCTTAGGGCAGAGGCCACCACATCTCTGC 69
Db 1 CTGACCCATCTCCAGCTCTTTGGCTGTCTTAGGGCAGAGGCCACCACATCTCTGC 50
QY 70 AGGCCAGCCAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 126
Db 61 AGAGCCAGTGAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 120
QY 127 CAGGACAGCCACCCAACTCTCACTATGCTGATGATGATGATGATGATGATGATG 186
Db 121 CAGGACAGCCACCCAACTCTCACTATGCTGATGATGATGATGATGATGATGATG 180
QY 187 GCGAGTCTTAGTGGCAGTGGGTCTGGGACAGACTTCACTCAACATCTCTCTGGAG 246
Db 181 GCGAGTCTTAGTGGCAGTGGGTCTGGGACAGACTTCACTCAACATCTCTCTGGAG 240
QY 247 GAGGAGGATGCTGCACTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 306
Db 241 GCTGATGATGCTGCACTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
QY 307 GCTGGGACCAAGCTGGAGCTGAAA 330
Db 301 GGAGGCTCCAAGCTGGAATCAA 324

RESULT 12
Bg107286 876 bp mRNA linear EST 26-JUN-2001
LOCUS
DEFINITION
IMAGE:502894285F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5039325 5', mRNA sequence.
ACCESSION
Bg107286
VERSION
Bg107286.1 GI:14558179
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 876)
AUTHORS
NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM1108 row: i column: 22
 High quality sequence stop: 823.
 Location/Qualifiers

FEATURES

1..876
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:5039325"
 /tissue type="spontaneous tumor, metastatic to mammary."
 Stem cell origin.
 /lab host="DH10B"
 /clone_lib="NCI CGAP Lu29"
 /note="Organ: Lung; Vector: pCMV-SPORT6; Site: 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
 BASE COUNT 239 a 242 c 192 g 203 t

Query Match 72.5%; Score 239.2; DB 12; Length 876;
 Best Local Similarity 85.8%; Pred. No. 4.9e-60;
 Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;
 QY 10 CTCACCAATCTCCAGCTTCTTTGGCTGTCTCTAGGGCAGAGGGCCACCATCTCTCGC 69
 DB 1 CTGACCCAAATCTCCAGCTTCTTTGGCTGTCTCTTAGGGCAGAGGGCCACCATCTCTCGC 60
 QY 70 AAGGCCAGCCAAAGTGTGATATGATGGTGATGTTATATG---TGGTACCAACAGAAA 126
 DB 61 AGAGCCAGTGAAGTGTGATGATGATGGCGATAGTTTATGCACTGGTACCAACAGAAA 120
 QY 127 CCAGGACAGCCACCACTCTCACCCTATGCTGCATCCATCTAGAACTGGGATCCCA 186
 DB 121 CTGACAGCAGCCACCACTCTCATTCTATCTTGGATCCAACTAGAACTGGGATCCCT 180
 QY 187 GCCAGTTTATGGCAGTGGGTCTGGGACAGACTTCACCTTCAACATCCATCTCTGTGGAG 246
 DB 181 GACAGTTTCAGTGGCAGTGGGTCTGGGACAGACTTCACCTTCAACATCTCTGTGGAG 240
 QY 247 GAGGAGATGCTGCACCTATCTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 306
 DB 241 GCTGATGATGCTGCAACCTATCTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
 QY 307 GCTGGGACCAAGCTGGAGCTGAAA 330
 DB 301 TCGGGACCAAGCTGGAGTAAA 324

RESULT 13
 BG967206
 LOCUS 602833889F1 NCI CGAP Co24 Mus musculus cDNA clone IMAGE:4988086 5',
 DEFINITION mRNA sequence.
 ACCESSION BG967206
 VERSION BG967206.1 GI:14354843
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 735)

AUTHORS

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM11000 row: b column: 23
 High quality sequence stop: 730.
 Location/Qualifiers

FEATURES

1..735
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:4988086"
 /lab host="DH10B (T1 phage-resistant)"
 /clone_lib="NCI CGAP Co24"
 /note="Organ: Colon; Vector: pCMV-SPORT6; Site: 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI CGAP Library."
 BASE COUNT 194 a 201 c 178 g 162 t

ORIGIN

Query Match 72.3%; Score 238.6; DB 12; Length 735;
 Best Local Similarity 84.4%; Pred. No. 6.7e-60;
 Matches 281; Conservative 0; Mismatches 49; Indels 3; Gaps 1;
 QY 1 GACATTGTCTCCAAATCTCCAGCTTCTTTGGCTGTCTCTAGGGCAGAGGGCCAC 60
 DB 86 GACATTGTCTCCAGCTTCTTTGGCTGTCTCTAGGGCAGAGGGCCAC 145
 QY 61 ATCTCTGCAAGCCAGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 117
 DB 146 ATCTCATGCAAGCCAGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 205
 QY 118 CAACAGAAACAGGAGCAGCCACCAACTCTCAGCTATGCTGCATCCAACTAGAACTCT 177
 DB 206 CAACAGAAACAGGAGCAGCCACCAAGCTCTCATCAAGTATGATCCGACTGGAATCT 265
 QY 178 GGGATCCCAAGCCAGGTTTGTAGTGGCAGTGGGTCTGGGACAGACTTCACCTCAACATCCAT 237
 DB 266 GGGGTCCCAAGCCAGGTTTGTAGTGGCAGTGGGTCTGGGACAGACTTCACCTCAACATCCAT 325
 QY 238 CCTGTGGAGGAGGAGTCTGCAACCTATTACTCTCAGCTTTGTAATGAGGATCCTCCC 297
 DB 326 CTTGTGGAGGAGGAGTCTGCAACATATTACTCTCAGCAGTTGGAGATTCCTCTC 385
 QY 298 ACGTTTCGGTGTGGGACCAAGCTGGAGCTGAAA 330
 DB 386 ACGTTTCGGTGTGGGACCAAGCTGGAGCTGAAA 418

RESULT 14

BG969552
 LOCUS 603303102F1 NCI CGAP Mam4 Mus musculus cDNA clone IMAGE:5348688 5',
 DEFINITION mRNA sequence.
 ACCESSION BG969552
 VERSION BG969552.1 GI:15573788
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 865)
 NIH-MGC http://mgc.nci.nih.gov/.

Db 302 CCTATGGAGGAGGATGATTCTGCAATGTATTTCTGTACGCAAAAGTAAGGAGGTTCTTTGG 361
QY 298 ACGTTCGGTCTGCTGGGACCAAGCTGGA 323
Db 362 ACGTTCGGTGGAGGCACGAGCTGGA 387

Search completed: January 14, 2004, 17:46:56
Job time : 1335.6 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 14, 2004, 15:55:45 ; Search time 40 Seconds
(without alignments)
3641.411 Million cell updates/sec

Title: US-09-759-112A-22
Perfect score: 330
Sequence: 1 gacattgtctcacaattc.....ggaccagaactggagctgaaa 330

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	294.6	89.3	396	2	US-08-483-636-1
2	294.6	89.3	396	2	US-08-483-632-1
3	286.6	86.8	333	1	US-08-491-845-7
4	283.4	85.9	393	3	US-08-579-378A-13
5	262.6	79.6	393	1	US-08-137-117D-32
6	262.6	79.6	393	1	US-08-436-717-32
7	261	79.1	333	1	US-08-275-053-10
8	261	79.1	333	1	US-08-275-053-16
9	261	79.1	363	1	US-08-111-080-21
10	261	79.1	363	1	US-08-211-980-21
11	261	79.1	363	5	PCT-US93-07967-21
12	257.8	78.1	339	2	US-08-553-497A-9
13	257.8	78.1	363	1	US-08-111-080-17
14	257.8	78.1	363	1	US-08-111-980-17
15	257.8	78.1	363	5	PCT-US92-07111-16
16	257.8	78.1	363	5	PCT-US93-07967-17
17	254.6	77.2	339	2	US-08-553-497A-5
18	249.8	75.7	393	1	US-07-634-278-66
19	249.8	75.7	393	1	US-08-477-728-66
20	249.8	75.7	393	1	US-08-474-040-66
21	249.8	75.7	393	1	US-08-487-200-66
22	249.8	75.7	393	2	US-08-621-751A-9
23	249.8	75.7	393	3	US-08-484-537-66
24	246.2	74.6	717	2	US-08-553-497A-17
25	245	74.2	906	2	US-08-656-906-24
26	245	74.2	906	3	US-09-217-847-24
27	243.4	73.8	333	1	US-08-442-542-3

28	243.4	73.8	333	3	US-08-765-469-3	Sequence 3, Appli
29	243.4	73.8	333	1	US-08-137-117D-24	Sequence 24, Appli
30	243.4	73.8	333	1	US-08-436-717-24	Sequence 24, Appli
31	243.4	73.8	1797	1	US-08-442-542-17	Sequence 17, Appli
32	243.4	73.8	1797	3	US-08-765-469-17	Sequence 17, Appli
33	242.4	73.5	783	4	US-08-487-283A-19	Sequence 19, Appli
34	239.4	72.5	333	1	US-08-207-169A-3	Sequence 3, Appli
35	238.6	72.3	336	3	US-09-065-059-14	Sequence 14, Appli
36	237	71.8	394	3	US-08-836-561-24	Sequence 24, Appli
37	237	71.8	394	4	US-09-434-122-24	Sequence 24, Appli
38	235.4	71.3	399	5	PCT-US94-14106-52	Sequence 52, Appli
39	235.4	71.3	428	3	US-08-589-939-4	Sequence 4, Appli
40	233.8	70.8	334	2	US-08-650-262-1	Sequence 1, Appli
41	233.8	70.8	723	5	PCT-US94-14106-56	Sequence 56, Appli
42	232.2	70.4	654	5	PCT-US96-13152-1	Sequence 1, Appli
43	231.4	70.1	332	3	US-08-881-037-58	Sequence 58, Appli
44	230.6	69.9	333	3	US-08-579-378A-17	Sequence 17, Appli
45	229	69.4	356	2	US-08-379-057-15	Sequence 15, Appli

ALIGNMENTS

RESULT 1
US-08-483-636-1
; Sequence 1, Application US/08483636
; Patent No. 5914110
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,636
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown

Best Local Similarity 88.9%; Pred. No. 2.9e-80;
Matches 296; Conservative 0; Mismatches 34; Indels 3; Gaps 1;

QY 1 GACATTGTGCTCACCAGTTCTCCAGCTTCTTTGGCTGTCTCTAGGGCAGAGGCCACC 60
Db 61 GACATTGTGTTGATCCAACTCCAGCTTCTTTGGCTGTCTCTAGGGCAGAGGCCACC 120

QY 61 ATCTCTGCAAGCCAGCCAGCAAGTGTGATTATGATGTTAGTATATG---TGGTAC 117
Db 121 ATATCTGCGAGAGCCAGTGAAGTGTGATGTTATGCAATAGTATGCACTGGTAC 180

QY 118 CAACAGAACCCAGGACAGCCACCAACTCTCAGCTATGCTGCAATCCAACTAGAAATCT 177
Db 181 CAGCAAAACCCAGGACAGCCACCAACTCTCAGCTATGCTGCAATCCAACTAGAAATCT 240

QY 178 GGGATCCAGCCAGGTTAGTGGCAGTGGTCTGGGACAGACTTCACCCCTCAACATCCAT 237
Db 241 CGGATCCCTGCCAGTTCAGTGGCAGTGGTCTAGGACAGACTTCACCCCTCACCATTAT 300

QY 238 CTGTGGAGGAGGATGCTGCAACCTATTACTGTAGCTTTGTAATGAGATCCTCCC 297
Db 301 CTGTGGAGGCTGATGATGTTCAACCTATTACTGTGCAAAAGTAAATGAGGATCCTCCC 360

QY 298 AGCTTCGGTCTGGGACCAAGCTGGAGCTGAAA 330
Db 361 ACCTTCGGTCTGGGACCAAGCTGGAGCTGAAA 393

RESULT 7
US-08-275-053-10
; Sequence 10, Application US/08275053
; Patent No. 5607847
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Recombinant human anti-human immunodeficiency
; virus antibody.
; NUMBER OF SEQUENCES: 16
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/275,053
; PRIOR APPLICATION NUMBER: PCT/GB93/01798
; APPLICATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 333 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
US-08-275-053-10

Query Match 79.1%; Score 261; DB 1; Length 333;
Best Local Similarity 88.6%; Pred. No. 9.4e-80;
Matches 295; Conservative 0; Mismatches 35; Indels 3; Gaps 1;

QY 1 GACATTGTGCTCACCAGTTCTCCAGCTTCTTTGGCTGTCTCTAGGGCAGAGGCCACC 60
Db 1 GACATTGTGCTGACCCAGTCTCCAGCTTCTTTGGCTGTCTCTAGGGCAGAGGCCACC 60

QY 61 ATCTCTGCAAGCCAGCCAGCAAGTGTGATTATGATGTTAGTATATG---TGGTAC 117
Db 61 ATATCTGCGAGAGCCAGTGAAGTGTGATGTTATGCAATAGTATGCACTGGTAC 120

QY 118 CAACAGAACCCAGGACAGCCACCAACTCTCAGCTATGCTGCAATCCAACTAGAAATCT 177
Db 121 CAGCAAAACCCAGGACAGTCAACCAACTCTCAGCTATGCTGCAATCCAACTAGAAATCT 180

QY 178 GGGATCCAGCCAGGTTAGTGGCAGTGGTCTGGGACAGACTTCACCCCTCAACATCCAT 237

Db 181 GGGGTCCCTCCAGGTTCACTGGCAGTGGTCTAGGACAGACTTCACCCCTCACCATTGAT 240

QY 238 CCTGTGGAGGAGAGATGCTGCAACTATTACTGTAGCTTTGTAATGAGGATCCTCCC 297

Db 241 CCTGTGGAGGCTGATGCTGCAACTATTACTGTGCAAAATAATGAGGATCCGCTC 300

QY 298 ACCTTCGGTCTGGGACCAAGCTGGAGCTGAAA 330

Db 301 ACCTTCGGTCTGGGACCAAGCTGGAGCTGAAA 333

RESULT 8
US-08-275-053-16/c
; Sequence 16, Application US/08275053
; Patent No. 5607847
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Recombinant human anti-human immunodeficiency
; virus antibody.
; NUMBER OF SEQUENCES: 16
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/275,053
; PRIOR APPLICATION NUMBER: PCT/GB93/01798
; APPLICATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 333 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
US-08-275-053-16

Query Match 79.1%; Score 261; DB 1; Length 333;
Best Local Similarity 88.6%; Pred. No. 9.4e-80;
Matches 295; Conservative 0; Mismatches 35; Indels 3; Gaps 1;

QY 1 GACATTGTGCTCACCAGTTCTCCAGCTTCTTTGGCTGTCTCTAGGGCAGAGGCCACC 60
Db 333 GACATTGTGCTGACCCAGTCTCCAGCTTCTTTGGCTGTCTCTAGGGCAGAGGCCACC 274

QY 61 ATCTCTGCAAGCCAGCCAGCAAGTGTGATTATGATGTTAGTATATG---TGGTAC 117
Db 273 ATATCTGCGAGAGCCAGTGAAGTGTGATGTTATGCAATAGTATGCACTGGTAC 214

QY 118 CAACAGAACCCAGGACAGCCACCAACTCTCAGCTATGCTGCAATCCAACTAGAAATCT 177
Db 213 CAGCAAAACCCAGGACAGTCAACCAACTCTCAGCTATGTTGCAATCCAACTAGAAATCT 154

QY 178 GGGATCCAGCCAGGTTAGTGGCAGTGGTCTGGGACAGACTTCACCCCTCAACATCCAT 237

Db 153 GGGGTCCCTCCAGGTTCACTGGCAGTGGTCTAGGACAGACTTCACCCCTCACCATTGAT 94

QY 238 CCTGTGGAGGAGAGATGCTGCAACCTATTACTGTAGCTTTGTAATGAGGATCCTCCC 297

Db 93 CCTGTGGAGGCTGATGCTGCAACCTATTACTGTGCAAAATAATGAGGATCCGCTC 34

QY 298 ACCTTCGGTCTGGGACCAAGCTGGAGCTGAAA 330

Db 33 ACCTTCGGTCTGGGACCAAGCTGGAGCTGAAA 1

RESULT 9
US-111-080-21
; Sequence 21, Application 08/111080
; Patent No. 555865
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya

Query Match	79.1%;	Score 261;	DB 1; Length 363;
Best Local Similarity	88.6%;	Pred. No. 9.8e-80;	
Matches 295;	Conservative 0;	Mismatches 35;	Indels 3; Gaps 1;

QY	1	GACATTGTGCTCACCAAATTC	CAGACTTCTTTGGCTGTCTCTAGGCAGAGGCCAACC	60
Dd	1	GCAATTGTGTGACCCCAATTC	CAGCTTCTTTGGCTGTCTCTAGGCAGAGGCCAACC	60
QY	61	ATCTCCTCGAAGGCCAGCCAAAGT	TTGATTATCATGCTGATAGTTATATG--TGTGTA	117
Dd	61	ATACTTCGCAGAGCCAGTGAAG	TGTGTATGTTATGGCAATAGTTTTATGCATCGGTAC	120
QY	118	CAACAGAAAACGAGACAGCACCA	ACCAACTCTCTACCTATGCTGCATCCAATCTAGAAATCT	177
Dd	121	CAGCAGAAAACGAGACAGTCAC	CCCAAACCTCTCATCTATGTTGCATCCAACCTAGAAATCT	180
QY	178	GGGATCCAGCCAGGTTTAGTGG	CAGAGTGGGTCTGGGACAGACTTCACCTCAACATCCAT	237
Dd	181	GGGGTCCCTGCACAGTTTCAG	TGGCAGTGGGTCTAGGACAGACTTTCACCTCACCATTGAT	240
QY	238	CCTCTGGAGGAGGAGGATGCTG	CACCTTATPACTGTGAGCTTTCTTAATAGGATCCTCCC	297
Dd	241	CCTGTGGAGGCTGATGATGCTG	CACCTTATPACTGTGAGCAAAATATAGGATCCCGTC	300
QY	298	ACGTTCCGTTGCTGGGACCAAG	CTGGAGCTGAAA	330

	Query Match	79.1%;	Score 261;	DB 1;	Length 363;
	Best Local Similarity	88.6%;	Pred. No. 9.8e-80;		
	Matches 295;	Conservative	0;	Mismatches 35;	Indels 3; Gaps 1;
Qy	1	GACATTGTGCTCACCAATCTCCAGCTCTCTTTGGCTGTGTCCTCAGGCAGAGGGCCACC	60		
Db	1	GACATTGTGCTGACCAATCTCCAGCTCTCTTTGGCTGTGTCCTCAGGCAGAGGGCCACC	60		
Qy	61	ATCTCTCGAAGCCAGCCAAAGTGTGATATGATGGTGTATAGTTATATG---TGGTAC	117		
Db	61	ATATCTCGAGCCAGTGAAGTGTGTAGTTATGGCAATAGTTTTATGCACTGGTAC	120		
Qy	118	CAACAGAAACCGAGCAGCCACCCAACTCTCCACTTATGCTGCATCCCAATCTAGAACTCT	177		
Db	121	CAGCAGAAACCGAGCAGTCACCCAAACCTCTCATCTATGTTCGATCCCAACCTAGAACTCT	180		
Qy	178	GGGATCCCAAGCCAGGTTTATGTGGCAGTGGGTCTGGGACAGACTTCACCCCTCAACATCCAT	237		

181	GGGGTCCCTCCGACAGCTTCAGTGGCAGTGGGTCTAGGACAGACATTCACCCCTCACCATTGAT	240
Db		
238	CTGTGTGAGGAGGAGGATGCTGCACCTATTACTGTCTCAGCTTTGTATATGAGGATCTCC	297
Qy		
241	CTGTGTGAGGAGGCTGATGATGCTGCACCTATTACTGTGAGCAAAATAATGAGGATCCGCTC	300
Db		
298	ACGTTTCGGTGTCTGGGACCAAGCTGAGCTGAAA	330
Qy		
301	ACGTTTCGGTGTCTGGGACCAAGCTGAGCTGAAA	333
Db		

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RESULT 11
PCT-US93-07967-21
; Sequence 21, Application PC/TUS9307967
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; TITLE OF INVENTION: HIV Immunotherapeutics
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07967

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Query Match	79.1%;	Score 261;	DB 5;	Length 363;
Best Local Similarity	88.6%;	Pred. No. 9.8e-80;		
Matches 295;	Conservative 0;	Mismatches 35;	Indels 3;	Gaps 1;

QY	1	GACATTGTCTCACAAATCTTCAGCTCTTTGGCTGTGTCCTAGGCAGAGGCCACC	60
Db	1	GACATTGTCTGACCCCAATCTTCAGCTCTTTGGCTGTGTCCTAGGCAGAGGCCACC	60
QY	61	ATCTCCTGCAGGCCAGCCAAAGTGTGATATATGATGGTGATAGTTATG---TGGTAC	117
Db	61	ATATCCTGCAGGCCAGTGAAGTGTGATAGTTATGGCAATAGTTTTATGCACCTGGTAC	120

QY	118	CAACAGAAAC	CAGGACAG	CACCAAACT	CCTCACC	TATGCTGCAT	CCAAATCT	AGAACT	177			
DB	121	CAGCAGAAAC	CAGGACAGT	CACCCAACT	CCTCAT	CTATGTTGCA	TCCAACT	AGAACT	180			
QY	178	GGGATCCCA	CAGCAGTT	TAGTGG	CAGTGGGT	CTGGGAC	AGACTT	CACCTCA	CAATCAT	237		
DB	181	GGGTCCTCG	CCAGGTT	CAGTGG	CAGTGGGT	CTAGGAC	AGACTT	CACCTC	CAATCAT	240		
QY	238	CCTGTGAG	GAGGAG	GATGCT	GCAACT	ATTACTGT	CAGCTTT	TGTAAT	CAGAGAT	CCTCC	297	
DB	241	CCTGTGAG	GGCTGAT	GTGATG	TCGCA	CCTATT	ACTGT	CAGCAAA	TAAAT	GAGGAT	TCGCTC	300
QY	298	ACGTTCCGT	GCTGGG	CAAC	AGCTGG	AGCTG	GAAG					330
DB	301	ACGTTCCGT	GCTGGG	CAAC	AGCTGG	AGCTG	GAAG					333

RESULT 12
US-08-553-497A-9
Sequence 9, Application US/08553497A
Patent No. 5844093
GENERAL INFORMATION:
APPLICANT: KETTLEBOROUGH, C. A.
APPLICANT: BENDIG, MARY M.
APPLICANT: ANSELL, KEITH H.
APPLICANT: GUSSOW, DETLEF
APPLICANT: ADAN, JAUME
APPLICANT: MITJANS, FRANCES
APPLICANT: ROSELL, ELISABET
APPLICANT: BLASCO, FRANCESC
APPLICANT: PIULATS, JAUME
TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD. SUITE 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497A
FILING DATE: 17-NOV-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/00978
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94118970.6
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna

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; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: mouse
; STRAIN: Balb/c
; DEVELOPMENTAL STAGE: adult
; TISSUE TYPE: Lymph node
; IMMEDIATE SOURCE:
; CLONE: L3 11D (light chain)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..339
; US-08-553-497A-9

Query Match      78.1%; Score 257.8; DB 2; Length 339;
Best Local Similarity 88.0%; Pred. No. 1.2e-78;
Matches 293; Conservative 0; Mismatches 37; Indels 3; Gaps 1;

QY 1 GACATTGTGCTCACCAGTTCACAGTTCCTTTGGCTGTGCTCTAGGGCAGAGGCCACC 60
DB 1 GACATTGAGCTCACCAGTTCACAGTTCCTTTGGCTGTGCTCTAGGGCAGAGGCCACC 60
QY 61 ATCTCTCTCAAGCCAGCCAGCAAGTGTGATGATGATGATGATGATGATGATGATG 117
DB 61 ATCTCTCTCCAGCCAGCCAGCAAGTGTGATGATGATGATGATGATGATGATGATG 120
QY 118 CAACAGAAACCCAGGACGCCACCAACTCTCTACCTATGCTGATGCTCAATCTAGAACT 177
DB 121 CAACAGAAACCCAGGACGCCACCAACTCTCTATCTATGCTGATGCTCAATCTAGAACT 180
QY 178 GGGATCCAGCCAGCTTTAGTGGCAGTGGGCTGGGACAGACTTCACCTCAACATCCAT 237
DB 181 GGGATCCCTGCAGCTTTAGTGGCAGTGGGCTGGGACAGACTTCACCTCAACATCCAT 240
QY 238 CTTGTGGAGGAGGAGTGTGCAACCTATTACTGTGAGCTTTTGTATAGGATCCCTCCC 297
DB 241 CTTGTGGAGGAGGAGTGTGCAACCTATTACTGTGAGCTTTTGTATAGGATCCCTCCC 300
QY 298 ACGTTCGGTGTGGACCAAGCTGGAGCTGAAA 330
DB 301 ACGTTCGGTGTGGACCAAGCTGGAGCTGAAA 333

RESULT 13
US-08-111-080-17
; Sequence 17, Application 08/111080
; Patent No. 555865
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; TITLE OF INVENTION: HIV Immunotherapeutics
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESS: Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/111,080
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/748,562
; FILING DATE: 22-AUG-1991
; PRIOR APPLICATION DATA:
```

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; APPLICATION NUMBER: PCT/US92/07111
; FILING DATE: 24-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,457
; FILING DATE: 22-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 31629
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 363 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..363
; US-08-111-080-17

Query Match      78.1%; Score 257.8; DB 1; Length 363;
Best Local Similarity 88.0%; Pred. No. 1.2e-78;
Matches 293; Conservative 0; Mismatches 37; Indels 3; Gaps 1;

QY 1 GACATTGTGCTCACCAGTTCCTCCAGCTTCCTTTGGCTGTGCTCTAGGGCAGAGGCCACC 60
DB 1 GACATTGTGCTCACCAGTTCCTCCAGCTTCCTTTGGCTGTGCTCTAGGGCAGAGGCCACC 60
QY 61 ATCTCTCTCAAGCCAGCCAGCAAGTGTGATGATGATGATGATGATGATGATGATG 117
DB 61 ATATCTCTGAGAGCCAGTGAAGTCTTGTATGATGATGATGATGATGATGATGATG 120
QY 118 CAACAGAAACCCAGGACGCCACCAACTCTCTACCTATGCTGATGCTCAATCTAGAACT 177
DB 121 CAGCAGAAACCCAGGACAGTCAACCTCTCTATGATGATGATGATGATGATGATGAT 180
QY 178 GGGATCCAGCCAGCTTTAGTGGCAGTGGGCTGGGACAGACTTCACCTCAACATCCAT 237
DB 181 GGGGTCCCTGCCAGCTTCAGTGGCAGTGGGCTGGGACAGACTTCACCTCAACATCCAT 240
QY 238 CTTGTGGAGGAGGAGTGTGCAACCTATTACTGTGAGCTTTTGTATAGGATCCCTCCC 297
DB 241 CTTGTGGAGGAGTGTGCAACCTATTACTGTGAGCTTTTGTATAGGATCCCTCCC 300
QY 298 ACGTTCGGTGTGGACCAAGCTGGAGCTGAAA 330
DB 301 GCGTTCGGTACTGGGACCAAGCTGGAGCTGAAA 333

RESULT 14
US-08-211-980-17
; Sequence 17, Application US/08211980
; Patent No. 566569
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; TITLE OF INVENTION: HIV Immunotherapeutics
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESS: Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

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;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/211,980
; FILING DATE:
;
; CLASSIFICATION: 424
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/07111
; FILING DATE: 24-AUG-1992
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,457
; FILING DATE: 22-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 31629
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
;
; TELEX: 25-3856
;
; INFORMATION FOR SEQ ID NO: 17:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 363 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
;
; FEATURE:
;
; NAME/KEY: CDS
; LOCATION: 1..363
;
; US-08-211-980-17

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Query Match	78.1%; Score 257.8; DB 1; Length 363;
Best Local Similarity	88.0%; Pred. No. 1.2e-78;
Matches 293; Conservative 0; Mismatches 37; Indels 3; Gaps 1;	
QY 1	GACATTGCTCCACCAATTCCTCCAGCTCTCTTGGCTGTCTCTTAGGGCAGAGGCCACCC 60
Db 1	
QY 1	GACATTGCTGACCCCAATCTCCAGCTCTTCTTGGCTGTCTCTTAGGGCAGAGGCCACCC 60
Db 1	
QY 61	ATCTCTCTCCAAAGGCCAGCCAAAGTGTATATGATGCTGGTGATAGTTATATG---TGGTAC 117
Db 61	ATATCTCTCAGACCCAGTGAAGTGTGATAGTTATGGCAATAGTTTATGCATGGTAC 120
QY 118	CAA CAGAAAC CAGGACAGCCACCAAACTCCTCACTATGCTGCATCCAACTTAGAATCT 177
Db 121	CAGCAGAAAC CAGGACAGCTACCCAACTCCTCATCTATGTTGCATCCAACTAGAATCT 180
QY 178	GGGATCC CAGCCAGGTTTATGTGGCAGTGGGTCTGGCAGACAGCTTCAACCTCAATCCAT 237
Db 181	GGGTCTCTCCAGGTTCAGTGGCAGTGGGTCTTAGCAGACAGCTTCAACCTCACCATTGAT 240
QY 238	CCTGTGGAGGAGGAGTGTGCCAACCTATTACTGTACGCTTTGTAAATGAGGATCCTCCC 297
Db 241	CCTGTGGAGGCTGATGATGCTGCACCTATTACTGTACGCAAAATTAATGAGATCCGCTC 300
QY 298	ACGTTCCGTTGCTGGGACCAAGCTGGAGCTGAAA 330
Db 301	CGCTTCGCTACTGGGACCAAGCTGGAGCTGAAA 333

RESULT 15
PCT-US92-07111-16
; Sequence 16, Application PC/TUS9207111
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; TITLE OF INVENTION: HIV Immunotherapeutics
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street

CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07111
FILING DATE: 19920824
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/748,562
FILING DATE: 22-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31016
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 363 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..363
PCT-US92-07111-16

Query Match	78.1%;	Score	257.8;	DB	5;	Length	363;	
Best Local Similarity	88.0%;	Pred. No.	1.2e-78;					
Matches	293;	Conservative	0;	Mismatches	37;	Indels	3;	
							Gaps	1;
<hr/>								
QY	1	GACATGTCACCA	ATTC	CCAGCTTC	TTGGCTGTCTCT	TAGGCGAGGGCCACC	60	
Db	1	GACATGTCGAC	CCCAAT	CTCCAGCTTC	TTGGCTGTCTCT	TAGGCGAGGGCCACC	60	
<hr/>								
QY	61	ATCTCTCGAAGG	CCGCCAAAGT	TTGATATGAT	TGGTGATGTTATATG	---TGGTAC	117	
Db	61	ATATCTCGAGAG	CCAGTGAAGT	TTGATGATG	TATGGCAATGTTTTATG	CACTGGTAC	120	
<hr/>								
QY	118	CACAGAAACAG	GACAGCAGC	CCCAACTCC	CACTATGTGTGCA	TCCAACTTAGAATCT	177	
Db	121	CAGCAGAAAC	CAGGACAGT	CACCAAACTCCT	CATCTATGTGCA	TCCAACTTAGAATCT	180	
<hr/>								
QY	178	GGGATCCACAG	CCAGT	TTAGTGCAGT	GGGTCTGGGACAGACTTC	CACCTCMAATCCAT	237	
Db	181	GGGTCCCTGC	AGTTTCAGT	GGCAGTGGGTCT	TAGGACAGACTTC	CACCTCACCATTGAT	240	
<hr/>								
QY	238	CCTGTGGAGGAG	GAGGATG	TGCCAACCTAT	TACTGTCA	GCTTTGTAATGAGGATCCTCCC	297	
Db	241	CCTGTGGAGG	CTGATG	TGCTCAACCTAT	TACTGTCA	GCAAAATATAGGATCCGCTC	300	
<hr/>								
QY	298	ACGTTCCGTG	CTGGACCAAG	CTGGAGCT	GGAA	330		
Db	301	CGCTTCGGT	TACTGGGACCAAG	CTGGAGCT	GGAA	333		

Search completed: January 14, 2004, 17:48:18
Job time : 42 secs

Query Match 83.5%; Score 275.4; DB 15; Length 768;
 Best Local Similarity 91.3%; Pred. No. 9.5e-85;
 Matches 304; Conservative 0; Mismatches 26; Indels 3; Gaps 1;

QY 1 GACATTGTGCTCACCACCAATCTCCAGCTCTTTGGCTGTCTCTAGGCGAGAGGCCACC 60
 DB 100 GACATTGTGCTCACCACCAATCTCCAGCTCTTTGGCTGTCTCTAGGCGAGAGGCCACC 159

QY 61 ATCTCTGCAAGCCAGCCAAAGTGTGATTATGATGAGTGTGATATG---TGGTAC 117
 DB 160 CTCTCTGCAAGCCAGCCAAAGTGTGATTATGATGAGTGTGATATG---TGGTAC 219

QY 118 CAACAGAAACCCAGGACAGCCAAAGTGTGATTATGATGAGTGTGATATG---TGGTAC 177
 DB 160 CTCTCTGCAAGCCAGCCAAAGTGTGATTATGATGAGTGTGATATG---TGGTAC 219

QY 178 GGGATCCAGCCAGCCAAAGTGTGATTATGATGAGTGTGATATG---TGGTAC 237
 DB 280 GGGATCCAGCCAGCCAAAGTGTGATTATGATGAGTGTGATATG---TGGTAC 237

QY 238 CCTGTGAGGAGGAGGATGCTGCAACCTATTACTGTGAGTGTGATATGAGGATCTCC 297
 DB 340 CCTGTGAGGAGGAGGATGCTGCAACCTATTACTGTGAGTGTGATATGAGGATCTCC 399

QY 298 ACGTTCGGTCTGGGACCAAGCTGGAGCTGAAA 330
 DB 400 ACGTTCGGTCTGGGACCAAGCTGGAGCTGAAA 432

RESULT 9
 US-10-384-933-51
 ; Sequence 51, Application US/10384933
 ; Publication No. US20030170817A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Serizawa, No. US20030170817A1ufusa
 ; APPLICANT: Haryuyama, Hideyuki
 ; APPLICANT: Nakahara, Kaori
 ; APPLICANT: Tamaki, Ikuko
 ; APPLICANT: Takahashi, Tohru
 ; TITLE OF INVENTION: Anti-Fas Antibodies
 ; FILE REFERENCE: 980126CIP/HG
 ; CURRENT APPLICATION NUMBER: US/10/384,933
 ; CURRENT FILING DATE: 2003-02-05
 ; PRIOR APPLICATION NUMBER: US/09/499,662
 ; PRIOR FILING DATE: 2000-02-09
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
 ; NUMBER OF SEQ ID NOS: 165
 ; SEQ ID NO 51
 ; LENGTH: 768
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (40)..(753)
 ; NAME/KEY: mat peptide
 ; LOCATION: (100)..(753)
 ; FEATURE:
 ; NAME/KEY: sig peptide
 ; LOCATION: (40)..(99)
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Designed DNA
 ; OTHER INFORMATION: encoding the light chain of humanized anti-human
 ; OTHER INFORMATION: Fas antibody
 US-10-384-933-51

Query Match 82.5%; Score 272.2; DB 13; Length 768;
 Best Local Similarity 90.7%; Pred. No. 1.2e-83;
 Matches 302; Conservative 0; Mismatches 28; Indels 3; Gaps 1;

QY 1 GACATTGTGCTCACCACCAATCTCCAGCTCTTTGGCTGTCTCTAGGCGAGAGGCCACC 60

DB 100 GACATTGTGCTCACCACCAATCTCCAGCTCTTTGGCTGTCTCTAGGCGAGAGGCCACC 159

QY 61 ATCTCTGCAAGCCAGCCAAAGTGTGATTATGATGAGTGTGATATG---TGGTAC 117
 DB 160 CTCTCTGCAAGCCAGCCAAAGTGTGATTATGATGAGTGTGATATG---TGGTAC 219

QY 118 CAACAGAAACCCAGGACAGCCAAAGTGTGATTATGATGAGTGTGATATG---TGGTAC 177
 DB 220 CAACAGAAACCCAGGACAGCCAAAGTGTGATTATGATGAGTGTGATATG---TGGTAC 219

QY 178 GGGATCCAGCCAGCCAAAGTGTGATTATGATGAGTGTGATATG---TGGTAC 237
 DB 280 GGGATCCAGCCAGCCAAAGTGTGATTATGATGAGTGTGATATG---TGGTAC 237

QY 238 CCTGTGAGGAGGAGGATGCTGCAACCTATTACTGTGAGTGTGATATGAGGATCTCC 297
 DB 340 CCTGTGAGGAGGAGGATGCTGCAACCTATTACTGTGAGTGTGATATGAGGATCTCC 399

QY 298 ACGTTCGGTCTGGGACCAAGCTGGAGCTGAAA 330
 DB 400 ACGTTCGGTCTGGGACCAAGCTGGAGCTGAAA 432

RESULT 10
 US-10-384-933-108
 ; Sequence 108, Application US/10384933
 ; Publication No. US20030170817A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Serizawa, No. US20030170817A1ufusa
 ; APPLICANT: Haryuyama, Hideyuki
 ; APPLICANT: Nakahara, Kaori
 ; APPLICANT: Tamaki, Ikuko
 ; APPLICANT: Takahashi, Tohru
 ; TITLE OF INVENTION: Anti-Fas Antibodies
 ; FILE REFERENCE: 980126CIP/HG
 ; CURRENT APPLICATION NUMBER: US/10/384,933
 ; CURRENT FILING DATE: 2003-02-05
 ; PRIOR APPLICATION NUMBER: US/09/499,662
 ; PRIOR FILING DATE: 2000-02-09
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
 ; NUMBER OF SEQ ID NOS: 165
 ; SEQ ID NO 108
 ; LENGTH: 768
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (40)..(753)
 ; NAME/KEY: mat peptide
 ; LOCATION: (100)..(753)
 ; FEATURE:
 ; NAME/KEY: sig peptide
 ; LOCATION: (40)..(99)
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Designed DNA
 ; OTHER INFORMATION: encoding the light chain of a humanized anti-Fas
 ; OTHER INFORMATION: antibody
 US-10-384-933-108

Query Match 82.5%; Score 272.2; DB 13; Length 768;
 Best Local Similarity 90.7%; Pred. No. 1.2e-83;
 Matches 302; Conservative 0; Mismatches 28; Indels 3; Gaps 1;

QY 1 GACATTGTGCTCACCACCAATCTCCAGCTCTTTGGCTGTCTCTAGGCGAGAGGCCACC 60
 DB 100 GACATTGTGCTCACCACCAATCTCCAGCTCTTTGGCTGTCTCTAGGCGAGAGGCCACC 159

QY 61 ATCTCTGCAAGCCAGCCAAAGTGTGATTATGATGAGTGTGATATG---TGGTAC 117
 DB 160 CTCTCTGCAAGCCAGCCAAAGTGTGATTATGATGAGTGTGATATG---TGGTAC 219

QY 118 CAACAGAAACAGGACAGCCACCCAACTCCTACCTATGCTGATCCAAATCTAGAAATCT 177
Db 220 CAACAGAAACAGGACAGCCACCCAGACTCTCTCATCTATGCTGATCCAAATCTGAAATCT 279
QY 178 GGGATCCAGACAGGTTTAGTGAGGAGTGGTCTGGGACAGACTTCAGCCTCAACATCCAT 237
Db 280 GGGATCCAGACAGGTTTAGTGAGGAGTGGTCTGGGACAGACTTCAGCCTCAACATCCAT 339
QY 238 CTTGTGGAGGAGGAGTCTGCAACCTATTACTGTCAGCTTTGTAATGAGGATCCTCC 297
Db 340 CTTGTGGAGGAGGAGTCTGCAACCTATTACTGTCAGCAAAAGTATGAGGATCCTCGG 399
QY 298 ACGTTCGGTCTGGACCAAGCTGAGCTGAAA 330
Db 340 CTTGTGGAGGAGGAGTCTGCAACCTATTACTGTCAGCAAAAGTATGAGGATCCTCGG 399
QY 298 ACGTTCGGTCTGGACCAAGCTGAGCTGAAA 330
Db 340 CTTGTGGAGGAGGAGTCTGCAACCTATTACTGTCAGCAAAAGTATGAGGATCCTCGG 399

RESULT 11

US-10-216-484-51
; Sequence 51, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030103976Alufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Takaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/216.484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 51
; LENGTH: 768

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: CDS
LOCATION: (40)..(753)
FEATURE:
NAME/KEY: mat peptide
LOCATION: (100)..(753)
FEATURE:
NAME/KEY: sig peptide
LOCATION: (40)..(99)
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Designed DNA
OTHER INFORMATION: encoding the light chain of humanized anti-human
OTHER INFORMATION: Fas antibody
US-10-216-484-51

Query Match 82.5%; Score 272.2; DB 15; Length 768;
Best Local Similarity 90.7%; Pred. No. 1.2e-83;
Matches 302; Conservative 0; Mismatches 28; Indels 3; Gaps 1;
QY 1 GACATTGTGCTCACCAGTCTCCAGCTTCTTTGGCTGTGCTCTAGGGCAGAGGGCCACC 60
Db 100 GACATTGTGCTCACCAGTCTCCAGTCTTTGTCTCTGCTCCAGGGGAGAGGGCCACC 159
QY 61 ATCTCTCTCAAGGCGCAGCAAAAGTGTGATTATGATGGTGTATATGAACTGTATATG 117
Db 160 CTCTCTCTCAAGGCGCAGCAAAAGTGTGATTATGATGGTGTATATGAACTGTATATG 219
QY 118 CAACAGAAACAGGACAGCCACCCAACTCCTACCTATGCTGATCCAAATCTAGAAATCT 177
Db 220 CAACAGAAACAGGACAGCCACCCAGACTCTCTCATCTATGCTGATCCAAATCTGAAATCT 279
QY 178 GGGATCCAGCAGGAGTCTGGGACAGACTTCAGCCTCAACATCCAT 237

Db 280 GGGATCCAGCAGGAGTCTGGGACAGACTTCAGCCTCAACATCCAT 339
QY 238 CTTGTGGAGGAGGAGTCTGCAACCTATTACTGTCAGCTTTGTAATGAGGATCCTCC 297
Db 340 CTTGTGGAGGAGGAGTCTGCAACCTATTACTGTCAGCAAAAGTATGAGGATCCTCGG 399
QY 298 ACGTTCGGTCTGGGACCAAGCTGAGCTGAAA 330
Db 400 ACGTTCGGTCAAGGCACCCAGGCTGGAATCAA 432

RESULT 12

US-10-216-484-108
; Sequence 108, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:

APPLICANT: Serizawa, No. US20030103976Alufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakahara, Kaori
APPLICANT: Tamaki, Ikuko
APPLICANT: Takahashi, Tohru

TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126CIP/HG
CURRENT APPLICATION NUMBER: US/10/216.484
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US/09/499,662
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: US 09/053,583
PRIOR FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 108
LENGTH: 768

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: CDS
LOCATION: (40)..(753)
FEATURE:

NAME/KEY: mat peptide
LOCATION: (100)..(753)
FEATURE:
NAME/KEY: sig peptide
LOCATION: (40)..(99)
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Designed DNA
OTHER INFORMATION: encoding the light chain of a humanized anti-Fas
OTHER INFORMATION: antibody
US-10-216-484-108

Query Match 82.5%; Score 272.2; DB 15; Length 768;
Best Local Similarity 90.7%; Pred. No. 1.2e-83;
Matches 302; Conservative 0; Mismatches 28; Indels 3; Gaps 1;
QY 1 GACATTGTGCTCACCAGTCTCCAGCTTCTTTGGCTGTGCTCTAGGGCAGAGGGCCACC 60
Db 100 GACATTGTGCTCACCAGTCTCCAGTCTTTGTCTCTGCTCCAGGGGAGAGGGCCACC 159
QY 61 ATCTCTCTCAAGGCGCAGCAAAAGTGTGATTATGATGGTGTATATGAACTGTATATG 117
Db 160 CTCTCTCTCAAGGCGCAGCAAAAGTGTGATTATGATGGTGTATATGAACTGTATATG 219
QY 118 CAACAGAAACAGGACAGCCACCCAACTCCTACCTATGCTGATCCAAATCTAGAAATCT 177
Db 220 CAACAGAAACAGGACAGCCACCCAGACTCTCTCATCTATGCTGATCCAAATCTGAAATCT 279
QY 178 GGGATCCAGCAGGAGTCTGGGACAGACTTCAGCCTCAACATCCAT 237
Db 280 GGGATCCAGCAGGAGTCTGGGACAGACTTCAGCCTCAACATCCAT 339
QY 238 CTTGTGGAGGAGGAGTCTGCAACCTATTACTGTCAGCTTTGTAATGAGGATCCTCC 297
Db 340 CTTGTGGAGGAGGAGTCTGCAACCTATTACTGTCAGCAAAAGTATGAGGATCCTCGG 399

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 14, 2004, 17:47:02 ; Search time 33.8095 Seconds
(without alignments)
516.420 Million cell updates/sec

Title: US-09-759-112A-24
Perfect score: 582
Sequence: 1 DIVTNSPASLAVSLGRAT.....COLCNEDEPPTFGATKLELK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues 1107863

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03:*

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2: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA1981.DAT.*

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4: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA1983.DAT.*

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22: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA2001.DAT.*

23: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA2002.DAT.*

24: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	582	100.0	110	AAO18536	Murine Mab 1F7 lig
2	537.5	92.4	132	AAO18536	Mouse Mab 3B9 lig
3	537.5	92.4	132	AAO18536	Light chain variab
4	537.5	92.4	132	AAO18536	Light chain sequen
5	532.5	91.5	111	AAO18536	Antibody 4H5 L cha
6	532.5	91.5	111	AAO18536	Murine derived pro
7	532.5	91.5	111	AAO18536	Murine derived pro
8	532.5	91.5	305	AAO18536	Antibody 4H5 L cha
9	532.5	91.5	305	AAO18536	Antibody 4H5 L cha

10	532.5	91.5	305	21	AAO18536	Murine derived pro
11	532.5	91.5	305	21	AAO18536	Murine derived pro
12	528.5	90.8	238	19	AAO18536	Anti-Fas Mab HF37A
13	528.5	90.8	238	21	AAO18536	Mouse anti-Fas ant
14	528.5	90.8	238	21	AAO18536	Humanised anti-Fas
15	528.5	90.8	238	21	AAO18536	Humanised anti-Fas
16	528.5	90.8	238	21	AAO18536	Humanised anti-Fas
17	526.5	90.5	238	23	AAO18536	Human penton base
18	526.5	90.5	238	24	AAO18536	Mouse DAV-1 light
19	526.5	90.5	238	24	AAO18536	Mouse anti-HIV mAb
20	522.5	89.8	111	15	AAO18536	Anti HIV antibody
21	521.5	89.6	131	14	AAO18536	Anti-CD4 antibody
22	519.5	89.3	111	10	AAO18536	Immunoglobulin L c
23	519.5	89.3	111	23	AAO18536	Mouse AC10 antibody
24	519.5	89.3	131	10	AAO18536	Amino acids sequen
25	515.5	88.6	113	22	AAO18536	Monoclonal antibody
26	512.5	88.1	232	18	AAO18536	MHI monoclonal ant
27	511.5	87.9	131	11	AAO18536	Anti-Peu 3a light
28	503.5	86.5	106	14	AAO18536	MAE15 light chain
29	503.5	86.5	106	21	AAO18536	Light chain amino
30	503.5	86.5	112	22	AAO18536	Anti-SAF-1 monoclo
31	498.5	85.7	103	21	AAO18536	Antibody 4H5 L cha
32	498.5	85.7	103	21	AAO18536	Murine derived pro
33	491.5	84.5	111	14	AAO18536	MAE11 light chain
34	491.5	84.5	111	21	AAO18536	Light chain amino
35	490.5	84.3	120	15	AAO18536	Sequence of the mo
36	487.5	83.8	218	24	AAO18536	TSH receptor antib
37	487.5	83.8	218	24	AAO18536	TSH receptor antib
38	487.5	83.8	238	19	AAO18536	Anti-Fas humanised
39	487.5	83.8	238	21	AAO18536	Humanised anti-Fas
40	487.5	83.8	238	21	AAO18536	Humanised anti-Fas
41	487.5	83.8	238	23	AAO18536	Humanised anti-Fas
42	487.5	83.8	238	23	AAO18536	Humanised anti-Fas
43	485.5	83.4	111	20	AAO18536	Mus musculus anti-
44	485.5	83.4	111	22	AAO18536	Variable light cha
45	476.5	81.9	238	19	AAO18536	Anti-Fas humanised

ALIGNMENTS

RESULT 1

AAO18536

ID AAO18536 standard; Protein; 110 AA.

AC AAO18536;

DT 11-OCT-2002 (first entry)

DE Murine Mab 1F7 light chain.

XX

XX Mouse; 1F7; antibody; immune modulator; anti-HIV antibody; CDR; complementarity determining region; framework-determining region; FR; heavy chain; light chain; HIV infection.

XX

OS Mus sp.

XX

PN WO200255668-A2.

XX

PD 18-JUL-2002.

XX

PF 11-JAN-2002; 2002WO-US00927.

XX

PR 11-JAN-2001; 2001US-0759112.

XX

XX (IMMP-) IMMOPHERON INC.

XX

XX Muller S, Kohler H;

XX

XX WPI; 2002-590668/63.

XX

XX N-PSDB; AAL48661.

XX

PT New polynucleotide encoding a complementarity- or framework-determining

PT region of an anti-idiotypic antibody that binds to human or primate
 PT anti-human immunodeficiency virus (HIV) antibodies, for use in
 PT vaccines against HIV -
 XX
 PS Claim 9; Page 23-24; 27pp; English.
 XX
 CC The present invention relates to coding sequences of the murine 1F7
 CC anti-idiotypic antibody complementarity-determining region (CDR) or
 CC framework-determining region (FR). The antibody binds to human or primate
 CC anti-human immunodeficiency virus (HIV) antibodies and can be used in the
 CC treatment of HIV infection. The present sequence is the 1F7 light chain.
 XX
 SQ Sequence 110 AA;

Query Match 100.0%; Score 582; DB 23; Length 110;
 Best Local Similarity 100.0%; Pred. No. 1.3e-42;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DIVLTNSPASLAVSLGQRATISCKASQSDVDGDSYMWYQKPGPPKLLTYAASNLESG 60
 DB 1 DIVLTNSPASLAVSLGQRATISCKASQSDVDGDSYMWYQKPGPPKLLTYAASNLESG 60
 QY 61 IPARESGSGSGTDFLTNIHPVEEEDAATYYCQLCNEPPTFGAGTKLELK 110
 DB 61 IPARESGSGSGTDFLTNIHPVEEEDAATYYCQLCNEPPTFGAGTKLELK 110

RESULT 2

AAAR70189
 ID AAR70189 standard; Protein; 132 AA.
 XX
 AC AAR70189;
 XX
 DT 25-MAR-2003 (updated)
 DT 20-SEP-1995 (first entry)
 XX
 DE Mouse MAb 3B9 light chain.
 XX
 KW Chimeric antibody; humanized antibody; antibody engineering;
 KW monoclonal antibody; MAb; interleukin-4; IL-4; allergy.

OS Mus sp.

FH Key Location/Qualifiers
 FT Peptide 1..20
 FT Region 44..58
 FT /label= CDR
 FT /note= "complementarity determining region"
 FT Region 74..80
 FT /label= CDR
 FT /note= "complementarity determining region"
 FT Region 113..121
 FT /label= CDR
 FT /note= "complementarity determining region"

XX WO9507301-A1.

XX 16-MAR-1995.

XX 07-SEP-1994; 94WO-US10308.

XX 07-SEP-1993; 93US-0117366.

PR 14-OCT-1993; 93US-0136783.

XX (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

XX Gross MS, Holmes SD, Sylvester DR;

XX WPI; 1995-123387/16.

DR N-PSDB; AAQ83490.

XX

PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
 PT from high affinity mAbs - useful in treatment of IL-4-mediated
 PT and IGE-mediated allergic conditions
 XX
 PS Disclosure; Fig.1; 97pp; English.
 XX
 CC Spleen cells from mice immunized with human IL-4 were used to prepare
 CC hybridomas, which were screened for anti-IL-4 Mab secretion. Only
 CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy
 CC chains were cloned into pGEM7f+ and transformed into E. coli
 CC DH5-alpha. The clones were sequenced (AAQ83490-91), and used for
 CC antibody engineering.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX

SQ Sequence 132 AA;
 Query Match 92.4%; Score 537.5; DB 16; Length 132;
 Best Local Similarity 93.7%; Pred. No. 1e-38;
 Matches 104; Conservative 1; Mismatches 5; Indels 1; Gaps 1;
 QY 1 DIVLTNSPASLAVSLGQRATISCKASQSDVDGDSYMWYQKPGPPKLLTYAASNLES 59
 DB 21 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYMWYQKPGPPKLLTYAASNLES 80
 QY 60 GIPARESGSGSGTDFLTNIHPVEEEDAATYYCQLCNEPPTFGAGTKLELK 110
 DB 81 GIPARESGSGSGTDFLTNIHPVEEEDAATYYCQSNEDPPTFGGKGLEIK 131

RESULT 3

AAAY23767
 ID AAY23767 standard; Protein; 132 AA.

XX AC AAY23767;

XX DT 13-SEP-1999 (first entry)

XX DE Light chain variable region of murine IL-4 antibody 3B9.

XX Light chain variable region; interleukin-4; IL-4; antibody 3B9;
 KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;
 KW immunoglobulin E-mediated allergic reaction; allergic rhinitis;
 KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
 KW rheumatoid arthritis; host-versus-graft disease; renal disease;
 KW allergy.

XX OS Mus sp.

XX PN US5928904-A.

XX 27-JUL-1999.

XX 07-JUN-1995; 95US-0483632.

XX 07-JUN-1995; 95US-0483632.

PR 07-SEP-1993; 93US-0117366.

PR 14-OCT-1993; 93US-0136783.

PR 07-SEP-1994; 94WO-US10308.

XX (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

XX Gross MS, Holmes SD, Sylvester DR;

XX WPI; 1999-429500/36.

DR N-PSDB; AAQ85884.

XX New DNA molecules encoding recombinant antibodies useful for

PT treating IL4-mediated conditions

XX Example 3; Fig 1; 50pp; English.

XX The present sequence represents the light chain variable region of

CC murine interleukin-4 (IL-4) antibody 3B9. The sequences are used
 CC in the production of chimeric and humanised IL-4 monoclonal antibodies.
 CC The antibodies of the invention are used in therapeutic and
 CC pharmaceutical compositions for treating IL-4 mediated and
 CC immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis,
 CC conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock,
 CC rheumatoid arthritis, host-versus-graft disease and renal disease.
 CC They are also useful in the diagnosis of an allergy or condition
 CC associated with excess IL-4 production through the measurement e.g. by
 CC ELISA of circulating endogenous IL-4 levels in humans.

XX
 SQ Sequence 132 AA;

Query Match 92.4%; Score 537.5; DB 20; Length 132;
 Best Local Similarity 93.7%; Pred. No. 1e-38; Indels 1; Gaps 1;
 Matches 104; Conservative 1; Mismatches 5;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSYVDYDGSYM-WYQKPGQPPKLLTYAASNLES 59
 |||||
 DB 21 DIVLTQSPASLAVSLGQRATISCKASQSYVDYDGSYMWYQKPGQPPKLLTYAASNLES 80
 |||||

QY 60 GIPARFSGSGTGDTFTLNHPVEEEDAATYYCOLCNEDEPPTFGAGTKLELK 110
 |||||
 DB 81 GIPARFSGSGTGDTFTLNHPVEEEDAATYYCQSNEDPPTFGGKTLEIK 131
 |||||

RESULT 4
 AAY18120
 ID AAY18120 standard; Protein; 132 AA.
 AC AAY18120;
 DT 11-AUG-1999 (first entry)
 DE Light chain sequence for murine 3B9 antibody.
 KW Antibody; interleukin-4; IL4; immunoglobulin E; IGE mediated disease;
 KW allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;
 KW atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;
 KW autoimmune disease; graft versus host disease.
 OS Mus sp.
 PN US5914110-A.
 XX
 XX 22-JUN-1999.
 PF 07-JUN-1995; 95US-0483636.
 PR 07-JUN-1995; 95US-0483636.
 PR 07-SEP-1993; 93US-0117366.
 PR 14-OCT-1993; 93US-0136783.
 PR 07-SEP-1994; 94WO-US10308.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Gross MS, Holmes SD, Sylvester DR;
 XX
 XX WPI; 1999-370482/31.
 DR N-PSDB; AAX79519.
 DR
 XX Recombinant IL4 antibodies
 PT
 XX Claim 24; Fig 1; 50pp; English.

CC This sequence represents the light chain of the murine 3B9
 CC antibody of the invention. The antibody is a chimeric or
 CC humanised interleukin-4 (IL4) monoclonal antibody for the treatment of
 CC immunoglobulin E (IGE) mediated diseases. The antibodies are useful for
 CC the treatment of allergic disorders such as allergic rhinitis,
 CC conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock.
 CC The antibodies are also useful for regulating B and T cell proliferation

CC and as such are useful in the treatment of autoimmune diseases and graft
 CC versus host disease.

XX
 SQ Sequence 132 AA;

Query Match 92.4%; Score 537.5; DB 20; Length 132;
 Best Local Similarity 93.7%; Pred. No. 1e-38; Indels 1; Gaps 1;
 Matches 104; Conservative 1; Mismatches 5;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSYVDYDGSYM-WYQKPGQPPKLLTYAASNLES 59
 |||||
 DB 21 DIVLTQSPASLAVSLGQRATISCKASQSYVDYDGSYMWYQKPGQPPKLLTYAASNLES 80
 |||||

QY 60 GIPARFSGSGTGDTFTLNHPVEEEDAATYYCOLCNEDEPPTFGAGTKLELK 110
 |||||
 DB 81 GIPARFSGSGTGDTFTLNHPVEEEDAATYYCQSNEDPPTFGGKTLEIK 131
 |||||

RESULT 5
 AAY59267
 ID AAY59267 standard; protein; 111 AA.
 AC AAY59267;
 XX
 XX 17-APR-2000 (first entry)
 DT
 DE Antibody 4H5 L chain fragment.
 XX
 XX CD4 antigen; anti-human; antibody; 4H5; drug.
 XX
 XX Mus sp.
 XX
 XX JPI1332563-A.
 PN
 XX 07-DEC-1999.
 PD
 XX 26-MAY-1998; 98JP-0163034.
 XX
 XX 26-MAY-1998; 98JP-0163034.
 PR
 XX (ASAH) ASAH KASEI KOGYO KK.
 PA
 XX WPI; 2000-091351/08.
 DR N-PSDB; AAZ58690.
 DR
 XX An antibody and the nucleic acid coding the antibody -
 PT
 XX Disclosure; Page 22-23; 25pp; Japanese.
 PS
 XX The invention provides an antibody having affinity to CD4 antigen. The
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and
 CC application for drugs. It is highly safe in human dose. The present
 CC sequence represents a L chain fragment of the antibody 4H5.

XX
 SQ Sequence 111 AA;

Query Match 91.5%; Score 532.5; DB 21; Length 111;
 Best Local Similarity 92.8%; Pred. No. 2.3e-38;
 Matches 103; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSYVDYDGSYM-WYQKPGQPPKLLTYAASNLES 59
 |||||
 DB 1 DIVLTQSPASLAVSLGQRATISCKASQSYVDYDGSYMWYQKPGQPPKLLTYAASNLES 60
 |||||

QY 60 GIPARFSGSGTGDTFTLNHPVEEEDAATYYCOLCNEDEPPTFGAGTKLELK 110
 |||||
 DB 61 GIPARFSGSGTGDTFTLNHPVEEEDAATYYCQSNEDPPTFGGKTLEIK 111
 |||||

RESULT 6
 AAY51144
 ID AAY51144 standard; Protein; 111 AA.
 XX

AC AAY51144;
 DT 31-MAR-2000 (first entry)
 XX Murine derived protein fragment #8.
 DE
 KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
 KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
 KW HIV infection; autoimmune disease; murine.
 XX
 OS Mus sp.
 XX WO9961629-A1.
 PN
 PD 02-DEC-1999.
 XX
 XX 24-MAY-1999; 99WO-JP02711.
 XX 25-MAY-1998; 98JP-0159957.
 XX 26-MAY-1998; 98JP-0163023.
 XX (ASAH) ASAH KASEI KOGYO KK.
 XX (ASAH) ASAH MEDICAL CO LTD.
 PA
 PI Ono M, Soka T, Morimoto I, Miyamura K;
 XX WPI; 2000-086720/07.
 XX
 XX 24-MAY-1999; 99WO-JP02711.
 XX 25-MAY-1998; 98JP-0159957.
 XX 26-MAY-1998; 98JP-0163023.
 XX (ASAH) ASAH KASEI KOGYO KK.
 XX (ASAH) ASAH MEDICAL CO LTD.
 PA
 PI Ono M, Soka T, Morimoto I, Miyamura K;
 XX WPI; 2000-086720/07.
 XX
 XX Devices containing antibodies recognising CD4 or CD34 and their use for
 PT the separation of CD4 or CD34 positive cells -
 XX
 XX Disclosure; Page 95; 111pp; Japanese.
 XX
 XX This invention describes a novel device (I) for separating cluster
 CC differentiation (CD)-positive cells using a recombinant (chimeric or
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful
 CC for the separation of CD4 or CD34 positive cells, which is useful for
 CC the collection of hematopoietic undifferentiated cells, elimination of
 CC lymphocytes from cells to be used in bone marrow transplantation, the
 CC detection of leukemic cells and the production of medicinal
 CC compositions for the treatment of HIV infection and autoimmune diseases.
 CC This sequence represents a murine derived protein fragment which is used
 CC to illustrate the method of the invention.
 XX
 XX Sequence 111 AA;
 SQ
 Query Match 91.5%; Score 532.5; DB 21; Length 111;
 Best Local Similarity 92.8%; Pred. No. 2.3e-38;
 Matches 103; Conservative 5; Mismatches 5; Indels 1; Gaps 1;
 QY 1 DIVLTNSPASLAVSLGQRATISCKASQSDVDGDSYM-WYQKPGQPPKLLTYAASNLES 59
 DB 1 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYMNWYQKPGQPPKLLTYAASNLES 60
 QY 60 GIPARFSGSGGTDFTLNHPVEEEDATYYCQLCNEDPPTFGAGTKLELK 110
 DB 61 GIPARFSGSGGTDFTLNHPVEEEDATYYCQSSSEDPPTFGGTKLEIK 111
 RESULT 7
 AAY51146
 ID AAY51146 standard; Protein; 111 AA.
 XX
 AC AAY51146;
 XX
 DT 31-MAR-2000 (first entry)
 XX Murine derived protein fragment #8.
 DE
 KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
 KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
 KW HIV infection; autoimmune disease; murine.
 XX

OS Mus sp.
 XX WO9961629-A1.
 PN
 PD 02-DEC-1999.
 XX
 XX 24-MAY-1999; 99WO-JP02711.
 XX 25-MAY-1998; 98JP-0159957.
 XX 26-MAY-1998; 98JP-0163023.
 XX (ASAH) ASAH KASEI KOGYO KK.
 XX (ASAH) ASAH MEDICAL CO LTD.
 PA
 PI Ono M, Soka T, Morimoto I, Miyamura K;
 XX WPI; 2000-086720/07.
 XX N-PSDB; AA244232.
 XX
 XX Devices containing antibodies recognising CD4 or CD34 and their use for
 PT the separation of CD4 or CD34 positive cells -
 XX
 XX Disclosure; Page 97-98; 111pp; Japanese.
 XX
 XX This invention describes a novel device (I) for separating cluster
 CC differentiation (CD)-positive cells using a recombinant (chimeric or
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful
 CC for the separation of CD4 or CD34 positive cells, which is useful for
 CC the collection of hematopoietic undifferentiated cells, elimination of
 CC lymphocytes from cells to be used in bone marrow transplantation, the
 CC detection of leukemic cells and the production of medicinal
 CC compositions for the treatment of HIV infection and autoimmune diseases.
 CC This sequence represents a murine derived protein fragment which is used
 CC to illustrate the method of the invention.
 XX
 XX Sequence 111 AA;
 SQ
 Query Match 91.5%; Score 532.5; DB 21; Length 111;
 Best Local Similarity 92.8%; Pred. No. 2.3e-38;
 Matches 103; Conservative 5; Mismatches 5; Indels 1; Gaps 1;
 QY 1 DIVLTNSPASLAVSLGQRATISCKASQSDVDGDSYM-WYQKPGQPPKLLTYAASNLES 59
 DB 1 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYMNWYQKPGQPPKLLTYAASNLES 60
 QY 60 GIPARFSGSGGTDFTLNHPVEEEDATYYCQLCNEDPPTFGAGTKLELK 110
 DB 61 GIPARFSGSGGTDFTLNHPVEEEDATYYCQSSSEDPPTFGGTKLEIK 111
 RESULT 8
 AAY59264
 ID AAY59264 standard; protein; 305 AA.
 XX
 AC AAY59264;
 XX
 DT 17-APR-2000 (first entry)
 XX
 XX Antibody 4H5 H chain sequence.
 XX
 XX CD4 antigen; anti-human; antibody; 4H5; drug.
 XX
 OS Mus sp.
 XX JP11332563-A.
 PN
 PD 07-DEC-1999.
 XX
 XX 26-MAY-1998; 98JP-0163034.
 XX 26-MAY-1998; 98JP-0163034.
 XX (ASAH) ASAH KASEI KOGYO KK.
 PA

AC AAY51142;
 DT 31-MAR-2000 (first entry)
 DE Murine derived protein fragment #4.
 KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
 KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
 KW HIV infection; autoimmune disease; murine.
 OS Mus sp.
 PN WO9961629-A1.
 PD 02-DEC-1999.
 PF 24-MAY-1999; 99WO-JP02711.
 PR 25-MAY-1998; 98JP-0159957.
 PR 26-MAY-1998; 98JP-0163023.
 XX (ASAH) ASAH KASEI KOGYO KK.
 PA (ASAH) ASAH MEDICAL CO LTD.
 PI Ono M, Soka T, Morimoto I, Miyamura K;
 DR WPI: 2000-086720/07.
 DR N-PSDB; AA244206.
 XX Devices containing antibodies recognising CD4 or CD34 and their use for
 PT the separation of CD4 or CD34 positive cells
 PT Claim 22; Page 82-84; 111pp; Japanese.
 CC This invention describes a novel device (I) for separating cluster
 CC differentiation (CD)-positive cells using a recombinant (chimeric or
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful
 CC for the separation of CD4 or CD34 positive cells, which is useful for
 CC the collection of hematopoietic undifferentiated cells, elimination of
 CC lymphocytes from cells to be used in bone marrow transplantation, the
 CC detection of leukemic cells and the production of medicinal
 CC compositions for the treatment of HIV infection and autoimmune diseases.
 CC This sequence represents a murine derived protein fragment which is used
 CC to illustrate the method of the invention.
 XX Sequence 305 AA;
 SQ Query Match 91.5%; Score 532.5; DB 21; Length 305;
 Best Local Similarity 92.8%; Pred. No. 6.3e-38;
 Matches 103; Conservative 2; Mismatches 5; Indels 1; Gaps 1;
 QY 1 DIVLTNSPASLAVSLGQRATISCKASQSDVDGDSYM-WYQKPGQPPKLLTYAASNL5 59
 DB 156 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYMWYQKPGQPPKLLTYAASNL5 215
 QY 60 GIPARFSGSGSDTFLNIHPVEEEDAAITYCQLCNEDEPPTFGAGTKLEIX 110
 DB 216 GIPARFSGSGSDTFLNIHPVEEEDAAITYCQLCNEDEPPTFGAGTKLEIX 266
 RESULT 12
 ID AAW83042 standard; Protein; 238 AA.
 AC AAW83042;
 XX 25-MAR-2003 (updated)
 DT 15-MAR-1999 (first entry)
 DE Anti-Fas MAb HFE7A light chain.
 XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
 KW

KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
 KW systemic lupus erythematosus; graft versus host disease;
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy; AIDS;
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 KW transplant rejection; therapy; complementarity determining region;
 CDR.
 XX
 XX Mus musculus.
 OS
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..20
 FT /label= sig_peptide
 FT Protein 21..238
 FT /label= Mat_protein
 FT Region 21..131
 FT /label= variable
 FT Region 132..238
 FT /label= Constant
 FT Region 44..58
 FT /label= CDR L1
 FT /note= "claim 9"
 FT Region 74..80
 FT /label= CDR L2
 FT /note= "claim 9"
 FT Region 113..121
 FT /label= CDR L3
 FT /note= "claim 9"
 XX
 XX AU9859701-A.
 XX
 PD 08-OCT-1998.
 XX
 PF 30-MAR-1998; 98AU-0059701.
 PR 08-OCT-1997; 97JP-0276064.
 PR 01-APR-1997; 97JP-0082953.
 PR 25-JUN-1997; 97JP-0169088.
 XX (SANY) SANKYO CO LTD.
 XX
 PI Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
 XX
 DR WPI: 1998-543440/01.
 DR N-PSDB; AAV701130.
 XX
 PT New antibodies and proteins bind conserved epitope of Fas antigen -
 PT used to evaluate drugs in animal models and to treat Fas-associated
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 PT myocarditis, hepatitis and AIDS
 XX
 PS Reference Example 4; Page 189-190; 292pp; English.
 XX
 CC This is the amino acid of the light chain of murine anti-human Fas
 CC monoclonal antibody HFE7A. cDNA (see AAV701130) encoding the light
 CC chain was obtained from HFE7A-secreting hybridoma (FERM BP-5828)
 CC RNA by RT-PCR (see AAV70127-28). The invention provides humanised
 CC HFE7A antibodies (see AAW83031-37) produced by CDR grafting. These
 CC antibodies are capable of inducing apoptosis in abnormal cells
 CC expressing Fas, and of inhibiting Fas-induced apoptosis in normal
 CC cells. They are used to evaluate, in animal models, treatments of
 CC diseases that involve Fas/Fas ligand interactions, and also to treat
 CC such diseases, including autoimmune disease (e.g. systemic lupus
 CC erythematosus, Hashimoto's disease, graft versus host disease,
 CC Sjogren syndrome, pernicious anaemia, Addison's disease,
 CC scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid
 CC arthritis, autoimmune haemolytic anaemia, sterility, myasthenia
 CC gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura

CC and insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
 CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
 CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).
 CC (Updated on 25-MAR-2003 to correct DR field.)
 XX
 SQ Sequence 238 AA;
 Query Match 90.8%; Score 528.5; DB 19; Length 238;
 Best Local Similarity 92.8%; Pred. No. 1.1e-37;
 Matches 103; Conservative 1; Mismatches 6; Indels 1; Gaps 1;
 QY 1 DIVLTNSPASLAVSLGQRATISCKASQSDYDGDSYM-WYQKPGQPPLKLLTYAASNLES 59
 DB 21 DIVLTQSPASLAVSLGQRATISCKASQSDYDGDSYMWYQKPGQPPLKLLTYAASNLES 80
 QY 60 GIPARFSGSGGTDFTLNHPVEEEDAAATYCOLCHNEDPTFGAGTKLEIK 110
 DB 81 GIPARFSGSGGTDFTLNHPVEEEDAAATYCOOSNEDPTFGGKTLEIK 131
 RESULT 13
 AAB14748
 ID AAB14748 standard; Protein; 238 AA.
 XX
 AC AAB14748;
 XX
 DT 24-NOV-2000 (first entry)
 XX
 DE Mouse anti-Fas antibody HFE7A light chain.
 XX
 KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
 KW murine; complementarity determining region; CDR; human Fas;
 KW Fas ligand; apoptosis modulator; programmed cell death;
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancyelophthisis;
 KW hepatitis; AIDS; Graft rejection; light chain.
 XX
 OS Mus musculus.
 XX
 PN JP2000169393-A.
 PD 20-JUN-2000.
 XX
 PF 30-SEP-1999; 99JP-0278301.
 XX
 PR 30-SEP-1998; 98JP-0276883.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 WPI: 2000-485645/43.
 DR N-PSDB; AAA72109.
 XX
 PT Preventive or treating agent for the diseases caused by an abnormality
 PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains
 PT anti-Fas antibody
 XX
 PS Example 4; Page 70; 139pp; Japanese.
 XX
 CC The invention relates to compositions for the prevention or treatment
 CC of diseases caused by an abnormality in the Fas/Fas ligand system
 CC containing an anti-Fas antibody as the active component. The anti-Fas
 CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
 CC or a humanised version of HFE7A containing identical CDRs
 CC (complementarity determining regions) to antibody HFE7A. Via its
 CC interaction with Fas, the antibody of the invention acts as a modulator
 CC of apoptosis. The compositions of the invention may therefore be used in
 CC the treatment or prevention of conditions such as autoimmune diseases,
 CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
 CC and organ graft rejection. The present sequence represents the
 CC light chain of the murine anti-human Fas monoclonal antibody HFE7A,
 CC which is produced by hybridoma HFE7A (FERM-BP-5828).
 XX

SQ Sequence 238 AA;
 Query Match 90.8%; Score 528.5; DB 21; Length 238;
 Best Local Similarity 92.8%; Pred. No. 1.1e-37;
 Matches 103; Conservative 1; Mismatches 6; Indels 1; Gaps 1;
 QY 1 DIVLTNSPASLAVSLGQRATISCKASQSDYDGDSYM-WYQKPGQPPLKLLTYAASNLES 59
 DB 21 DIVLTQSPASLAVSLGQRATISCKASQSDYDGDSYMWYQKPGQPPLKLLTYAASNLES 80
 QY 60 GIPARFSGSGGTDFTLNHPVEEEDAAATYCOLCHNEDPTFGAGTKLEIK 110
 DB 81 GIPARFSGSGGTDFTLNHPVEEEDAAATYCOOSNEDPTFGGKTLEIK 131
 RESULT 14
 AAW90898
 ID AAW90898 standard; Protein; 238 AA.
 XX
 AC AAW90898;
 XX
 DT 08-AUG-2000 (first entry)
 XX
 DE Murine anti-Fas antibody HFE7A light chain protein.
 XX
 KW Fas: antibody; murine; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus; HFE7A;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 XX
 OS Mus musculus.
 XX
 PN EP990663-A2.
 XX
 PD 05-APR-2000.
 XX
 PF 29-SEP-1999; 99EP-0307711.
 XX
 PR 30-SEP-1998; 98JP-0276881.
 PR 30-SEP-1998; 98JP-0276882.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 WPI: 2000-258930/23.
 DR N-PSDB; AAA11547.
 XX
 PT New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems
 XX
 PS Example reference 4; Page 104; 263pp; English.
 XX
 CC This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic

CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a murine anti-Fas monoclonal antibody HPE7A light chain described in the
 CC method of the invention.

XX
 SQ Sequence 238 AA;

Query Match 90.8%; Score 528.5; DB 21; Length 238;
 Best Local Similarity 92.8%; Pred. No. 1.1e-37;
 Matches 103; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSVYDGDYSY-WYQKPGQPPKLLTYAASNLES 59
 DB 21 DIVLTQSPASLAVSLGORATISCKASQSVYDGDYSYMWYQKPGQPPKLLTYAASNLES 80
 QY 60 GIPARFSGSGGTDFTLNHPVEEEDAAATYQCQNSNEDPRTFGGKLEIK 110
 DB 81 GIPARFSGSGGTDFTLNHPVEEEDAAATYQCQNSNEDPRTFGGKLEIK 131

RESULT 15
 ABB74867
 ID ABB74867 standard; Peptide; 238 AA.
 XX AC ABB74867;
 DT 26-APR-2002 (first entry)
 XX Humanised anti-Fas antibody related peptide SEQ ID NO 33.
 DE Human; mouse; humanised anti-Fas antibody; Fas/Fas ligand;
 KW light chain subunit; apoptosis; immunosuppressive; antiallergic;
 KW autoimmune disease; allergy; atopic.
 XX OS Homo sapiens.
 XX JP2001342148-A.
 XX PD 11-DEC-2001.
 XX 28-MAR-2001; 2001JP-0093106.
 XX 29-MAR-2000; 2000JP-0090918.
 XX (SANYO) SANKYO CO LTD.
 XX WPI; 2002-145113/19.
 XX Drug containing humanised anti-Fas antibody, used for preventing and
 PT treating autoimmune diseases, allergy, and atopy -
 XX Example 6 (Preparatory); Page 26; 194pp; Japanese.

The invention relates to a preventive or treating agent for diseases
 caused by abnormality in Fas/Fas ligand system containing as the active
 component an antibody having as the light chain subunit a polypeptide
 containing residues 1-218 of one of 3, 239 residue amino acid sequences,
 or residues 1-451 of one of 3, 470 residue amino acid sequences, all
 fully defined in the specification and having an activity of combining
 specifically with mammalian Fas and an activity of inducing apoptosis
 in a cell expressing Fas. The agent has immunosuppressive and
 CC antiallergic activity and is used for preventing and treating autoimmune

CC diseases, allergy, atopy and others. The present sequence is that of a
 CC peptide, useful to the invention.

XX
 SQ Sequence 238 AA;

Query Match 90.8%; Score 528.5; DB 23; Length 238;
 Best Local Similarity 92.8%; Pred. No. 1.1e-37;
 Matches 103; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSVYDGDYSY-WYQKPGQPPKLLTYAASNLES 59
 DB 21 DIVLTQSPASLAVSLGORATISCKASQSVYDGDYSYMWYQKPGQPPKLLTYAASNLES 80
 QY 60 GIPARFSGSGGTDFTLNHPVEEEDAAATYQCQNSNEDPRTFGGKLEIK 110
 DB 81 GIPARFSGSGGTDFTLNHPVEEEDAAATYQCQNSNEDPRTFGGKLEIK 131

Search completed: January 14, 2004, 19:11:26
 Job time : 35.8095 secs

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OM protein - protein search, using sw model

Run on: January 14, 2004, 19:02:07 ; Search time 14.7619 Seconds
(without alignments)
716.612 Million cell updates/sec

Title: US-09-759-112A-24
Perfect score: 582
Sequence: 1 DIVLTNSPASLAVSLQGRAT.....COLCNEDEPTFGAGTKLELK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	533.5	91.7	111	1 KVM583	Ig kappa chain V r
2	527.5	90.6	111	1 KVM543	Ig kappa chain V r
3	523.5	89.9	111	1 KVM508	Ig kappa chain V r
4	521.5	89.6	112	2 S19971	Ig kappa chain V r
5	521.5	89.6	131	2 PH1226	Ig kappa chain pre
6	520.5	89.4	111	1 KVM569	Ig kappa chain V r
7	505	86.8	110	1 KVM510	Ig kappa chain V r
8	503.5	86.5	111	1 KVM5C1	Ig kappa chain V r
9	502.5	86.3	112	2 S19976	Ig kappa chain V r
10	485.5	83.4	112	2 S19972	Ig kappa chain V r
11	476.5	81.9	111	2 S09966	Ig kappa chain V r
12	473.5	81.4	111	1 KVM575	Ig kappa chain V-J
13	470.5	80.8	111	1 KVM540	Ig kappa chain V r
14	468.5	80.5	111	1 KVM584	Ig kappa chain V r
15	457.5	78.6	112	2 S45715	Ig kappa chain V r
16	455.5	78.3	111	1 KVM537	Ig kappa chain V r
17	454.5	78.1	111	1 KVM585	Ig kappa chain V r
18	452.5	77.7	131	2 S5027	Ig kappa chain V r
19	451.5	77.6	210	2 A56169	Ig light chain pre
20	449.5	77.2	218	2 J25810	Ig kappa chain V r
21	448.5	77.1	131	1 KVM5M6	monoclonal antibody
22	445.5	76.5	218	2 S68241	Ig kappa chain pre
23	442.5	76.0	115	2 S63596	Ig kappa chain V r
24	441.5	75.9	93	2 A38601	Ig kappa chain V r
25	438.5	75.3	111	2 S09963	Ig kappa chain V-J
26	438.5	75.3	111	2 D45722	Ig kappa chain V r
27	432.5	74.3	111	1 KVM580	anti-glycoprotein
28	430.5	74.0	107	2 S26343	Ig kappa chain V r
29	430.5	74.0	107	2 S26344	Ig kappa chain V r

ALIGNMENTS

RESULT 1

KVM583
Ig kappa chain V region (PC7183) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
C/Accession: B01937; A01937
R/Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A/Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A/Reference number: A93204; MUID:79073152; PMID:103003
A/Accession: B01937
A/Molecule type: protein
A/Residues: 1-111 <WEI>
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 1 C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IM>
F:23-92/Disulfide bonds: #status predicted

Query Match 91.7%; Score 533.5; DB 1; Length 111;
Best Local Similarity 94.6%; Pred. No. 2.6e-41;
Matches 105; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
Qy 1 DIVLTNSPASLAVSLQGRATISCKASQSDYDGDSTV-WYQKPGQPPKLLTYAASNLIS 59
Db 1 DIVLTQSPASLAVSLQGRATISCKASQSDYDGDSTVWYQKPGQPPKLLTYAASNLIS 60
Qy 60 GIPARFSGSGGDTFTLNHPVEEEDAAATYYCQCNEDPTFGAGTKLELK 110
Db 61 GIPARFSGSGGDTFTLNHPVEEEDAAATYYCQSNEDPLTFGAGTKLELK 111

RESULT 2

KVM543
Ig kappa chain V region (PC7043) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 21-Jan-2000
C/Accession: A01937; S42187; S42194; S42190; S42189; S42188; S42191; S42192
R/Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A/Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A/Reference number: A93204; MUID:79073152; PMID:103003
A/Accession: A01937
A/Molecule type: protein
A/Residues: 1-111 <WEI>
R/Mo, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A/Title: Variable region gene selection of immunoglobulin G-expressing B cells with spe
A/Reference number: S42176; MUID:94009207; PMID:7691608
A/Accession: S42187
A/Molecule type: DNA

Matches 100; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSDYDGDSDYM-WYQKPGOPPKLLTYAASNLES 59

Db 21 DIVLTQSPASLPSLGLORATISCKASQSLDYDGDSDYMWYQKPGOPPKLLTYAASNLES 80

QY 60 GIPARFSGSGSGDFTLNHPVEEEDAATYQCQSNEDPPTFGAGTKLEK 110

Db 81 GIPARFSGSGSGDFTLNHPVEEEDAATYQCQSNEDPPTFGAGTKLEK 131

RESULT 6

KVMS69

Ig kappa chain V region (PC7210) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000

C:Accession: E01937; A01937

R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.

Nature 276, 785-790, 1978

A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.

A:Reference number: A93204; MUID:79073152; PMID:103003

A:Accession: E01937

A:Molecule type: protein

A:Residues: 1-111 <WEI>

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger disulfide bonds.

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-94/Domain: immunoglobulin homology <IMM>

F:23-92/Disulfide bonds: #status predicted

Query Match 89.4%; Score 520.5; DB 1; Length 111;

Best Local Similarity 91.0%; Pred. No. 3.8e-40;

Matches 101; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSDYDGDSDYM-WYQKPGOPPKLLTYAASNLES 59

Db 1 DIVLTQSPASLAVSLGORATISCKASQSDYDGDSDYMWYQKPGOPPKLLTYAASNLES 60

QY 60 GIPARFSGSGSGDFTLNHPVEEEDAATYQCQSNEDPPTFGAGTKLEK 110

Db 61 GIPARFSGSGSGDFTLNHPVEEEDAATYQCQSNEDPPTFGAGTKLEK 111

RESULT 7

KVMS10

Ig kappa chain V region (PC7210) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000

C:Accession: D01937; A01937

R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.

Nature 276, 785-790, 1978

A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.

A:Reference number: A93204; MUID:79073152; PMID:103003

A:Accession: D01937

A:Molecule type: protein

A:Residues: 1-110 <WEI>

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger disulfide bonds.

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-94/Domain: immunoglobulin homology <IMM>

F:23-92/Disulfide bonds: #status predicted

Query Match 86.8%; Score 505; DB 1; Length 110;

Best Local Similarity 90.1%; Pred. No. 9.4e-39;

Matches 100; Conservative 4; Mismatches 5; Indels 2; Gaps 2;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSDYDGDSDYM-WYQKPGOPPKLLTYAASNLES 59

Db 1 DIVLTQSPASLAVSLGORATISCKASQSLDYDGDSDYMWYQKPGOPPKLLTYAASNLES 60

QY 60 GIPARFSGSGSGDFTLNHPVEEEDAATYQCQSNEDPPTFGAGTKLEK 110

Db 61 GIPARFSGSGSGDFTLNHPVEEEDAATYCHQ-SEDPWTFSGTKLEIK 110

RESULT 8

KVMSCL

Ig kappa chain V region (CBPC 101) - mouse (tentative sequence)

C:Species: Mus musculus (house mouse)

C>Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 31-Mar-2000

C:Accession: A01936

R:McKean, D.J.; Bell, M.; Potter, M.

Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978

A:Title: Mechanisms of antibody diversity: multiple genes encode structurally related m

A:Reference number: A93822; MUID:79012520; PMID:99744

A:Accession: A01936

A:Molecule type: protein

A:Residues: 1-111 <MCK>

C:Comment: This chain was isolated from a myeloma protein.

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger disulfide bonds.

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer

F:16-94/Domain: immunoglobulin homology <IMM>

F:23-92/Disulfide bonds: #status predicted

Query Match 86.5%; Score 503.5; DB 1; Length 111;

Best Local Similarity 89.2%; Pred. No. 1.3e-38;

Matches 99; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSDYDGDSDYM-WYQKPGOPPKLLTYAASNLES 59

Db 1 DIVLTQSPASLAVSLGORATISCKASQSDYDGDSDYMWYQKPGOPPKLLTYAASNLES 60

QY 60 GIPARFSGSGSGDFTLNHPVEEEDAATYQCQSNEDPPTFGAGTKLEK 110

Db 61 GIPARFSGSGSGDFTLNHPVEEEDAATYQCQSNEDPPTFGAGTKLEK 111

RESULT 9

SI9976

Ig kappa chain V region (M-T413) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000

C:Accession: SI9976

R:Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.

submitted to the EMBL Data Library, March 1992

A:Description: Structural characterization of CD4 mAb.

A:Reference number: SI9963

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-112 <WEI>

A:Cross-references: EMBL:X65093; NID:g52298; PIDN:CAA46221.1; PID:g52299

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-94/Domain: immunoglobulin homology <IMM>

F:23-92/Disulfide bonds: #status predicted

Query Match 86.3%; Score 502.5; DB 2; Length 112;

Best Local Similarity 88.3%; Pred. No. 1.6e-38;

Matches 98; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSDYDGDSDYM-WYQKPGOPPKLLTYAASNLES 59

Db 1 DIVLTQSPASLAVSLGORATISCKASQSLDYDGDSDYMWYQKPGOPPKLLTYAASNLES 60

QY 60 GIPARFSGSGSGDFTLNHPVEEEDAATYQCQSNEDPPTFGAGTKLEK 110

Db 61 GIPARFSGSGSGDFTLNHPVEEEDAATYQCQSNEDPPTFGAGTKLEK 111

RESULT 10

SI9972

Ig kappa chain V region (M-T321) - mouse (fragment)


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Query Match      80.5%; Score 468.5; DB 1; Length 111;
Best Local Similarity 83.8%; Pred. No. 1.9e-35;
Matches 93; Conservative 4; Mismatches 13; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSYVDGDSYM-WYQKPGQPPKLLTYAASNLES 59
   |||||
Db 1 DIVLTQSPASLAVSLGQRATISCRASKSVSTSGSYNHWYQKPGQPPKLLIYLASNLES 60
   |||||

QY 60 GIPARFSGSGGTDFTLNTHPVEEEDAATYYCOLCNEDEPTFGAGTKLEK 110
   |||||
Db 61 GVPARFSGSGGTDFTLNTHPVEEEDAATYYQHSRELPRTFGGGKLEIK 111
   |||||

RESULT 15
S45715
IG kappa chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 14-Nov-1997 #text_change 07-May-1999
C:Accession: S45715
R:Kim, H.H.; Kato, K.; Yanato, S.; Igarashi, T.; Matsunaga, C.; Ohtsuka, H.; Higuchi, A.
FERS Lett. 346, 246-250, 1994
A:Title: Application of (13)C NMR spectroscopy to paratope mapping for larger antigen-Pe
A:Reference number: S45714; MUID:94283606; PMID:8013642
A:Accession: S45715
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-112 <KIM>
A:Experimental source: cell line Ex-3C7
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match      78.6%; Score 457.5; DB 2; Length 112;
Best Local Similarity 82.0%; Pred. No. 1.8e-34;
Matches 91; Conservative 6; Mismatches 13; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSYVDGDSYM-WYQKPGQPPKLLTYAASNLES 59
   |||||
Db 1 DIVLTQSPASLAVSLGQRATISCRASKSVSTSGSYNHWYQKPGQPPKLLIYLASNLES 60
   |||||

QY 60 GIPARFSGSGGTDFTLNTHPVEEEDAATYYCOLCNEDEPTFGAGTKLEK 110
   |||||
Db 61 GVPARFSGSGGTDFTLNTHPVEEEDAANYHCQHSRDLPLTFGAGTKLEK 111
   |||||

Search completed: January 14, 2004, 19:13:48
Job time : 15.7619 secs

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 14, 2004, 17:48:21 ; Search time 10 Seconds
(without alignments)
517.294 Million cell updates/sec

Title: US-09-759-112a-24

Perfect score: 582

Sequence: 1 DIVLTNSPASLAVSLGORAT.....COLCNEDEPTFGAGTKLELK 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 segs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	533.5	91.7	111	1	KV3N_MOUSE
2	527.5	90.6	111	1	KV3M_MOUSE
3	523.5	89.9	111	1	KV3O_MOUSE
4	520.5	89.4	111	1	KV3Q_MOUSE
5	505	86.8	110	1	KV3P_MOUSE
6	503.5	86.5	111	1	KV3L_MOUSE
7	473.5	81.4	111	1	KV3S_MOUSE
8	470.5	80.8	111	1	KV3T_MOUSE
9	468.5	80.5	111	1	KV3R_MOUSE
10	455.5	78.3	111	1	KV3H_MOUSE
11	455.5	78.3	111	1	KV3K_MOUSE
12	454.5	78.1	111	1	KV3U_MOUSE
13	449.5	77.2	111	1	KV3J_MOUSE
14	448.5	77.1	131	1	KV3I_MOUSE
15	435.5	74.8	111	1	KV3C_MOUSE
16	433	74.4	112	1	KV3B_MOUSE
17	432.5	74.3	111	1	KV3A_MOUSE
18	430.5	74.0	108	1	KV3V_MOUSE
19	428.5	73.6	111	1	KV3D_MOUSE
20	424.5	72.9	112	1	KV3G_MOUSE
21	424.5	72.9	132	1	KV3F_MOUSE
22	392.5	67.4	111	1	KV3E_MOUSE
23	373.5	64.2	114	1	KV4E_HUMAN
24	371.5	63.8	134	1	KV4C_HUMAN
25	366	62.9	133	1	KV4B_HUMAN
26	352.5	60.6	108	1	KV5P_MOUSE
27	351	60.3	129	1	KV3H_HUMAN
28	350.5	60.2	108	1	KV1M_HUMAN
29	344	59.1	109	1	KV3D_HUMAN
30	343	58.9	129	1	KV3L_HUMAN
31	340	58.4	109	1	KV3F_HUMAN
32	339	58.2	109	1	KV3B_HUMAN
33	337.5	58.0	108	1	KV1K_HUMAN

34	337.5	58.0	129	1	KV1W_HUMAN	P04431	homo sapien
35	336	57.7	129	1	KV3M_HUMAN	P18136	homo sapien
36	335.5	57.6	108	1	KV1H_HUMAN	P01600	homo sapien
37	333.5	57.3	108	1	KV1N_HUMAN	P01606	homo sapien
38	333	57.2	113	1	KV2G_MOUSE	P01631	mus musculus
39	331.5	57.0	108	1	KV1F_HUMAN	P01598	homo sapien
40	331.5	57.0	108	1	KV1G_HUMAN	P01599	homo sapien
41	329.5	56.6	121	1	KV4O_HUMAN	P06312	homo sapien
42	328.5	56.4	108	1	KV1B_HUMAN	P01594	homo sapien
43	328	56.4	133	1	KV2E_HUMAN	P06310	homo sapien
44	327.5	56.3	108	1	KV1E_HUMAN	P01597	homo sapien
45	327	56.2	109	1	KV3E_HUMAN	P01623	homo sapien

ALIGNMENTS

RESULT 1
KV3N_MOUSE STANDARD; PRT; 111 AA.
AC P01666;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7183.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE
RX MEDLINE=79073152; PubMed=103003;
RA Waigert M., Gammatan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
XT diversity.";
RL Nature 276:785-790(1978).
DR HIR; B01937; KVM83.
DR HSP; P01679; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11952 MW; 2058BB50CE306D31 CRC64;

Query Match 91.7%; Score 533.5; DB 1; Length 111;

Best Local Similarity 94.6%; Pred. No. 1.8e-46;

Matches 105; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSVYDGDGYSY-WYQKPGQPPKLLTYAASNLES 59

Db 1 DIVLTQSPASLAVSLGORATISCKASQSVYDGDGYSYNNWYQKPGQPPKLLTYAASNLES 60

QY 60 GIPARFSGSGGTDTFLNIHPVEEEDATYTCOLCNEDEPTFGAGTKLELK 110

Db 61 GIPARFSGSGGTDTFLNIHPVEEEDATYTCQSQNEDEPTFGAGTKLELK 111

RESULT 2

KV3M_MOUSE

ID KV3M_MOUSE STANDARD; PRT; 111 AA.

AC P01665;

DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region PC 7043.
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 diversity.";
 RL Nature 276:785-790(1978).
 DR HSSP; P80362; IWL.
 DR InterPro; IPR007110; Ig-Like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS0835; IG_LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 111
 FT DISULFID 23 92
 FT NON TER 111 111
 SQ SEQUENCE 111 AA; 12002 MW; 7A5FCB586C306D29 CRC64;

Query Match 90.8%; Score 527.5; DB 1; Length 111;

Best Local Similarity 92.8%; Pred. No. 7.2e-46;

Matches 103; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSDYDGDSYM-WYQKPGQPPKLLTYAASNLES 59
 DB 1 DIVLTQSPASLAVSLGORATISCKASQSDYDGDSYM-WYQKPGQPPKLLTYAASNLES 60
 QY 60 GIPARFSGSGGDTFTLNHPVEEEDAATYCOLCNEDEPTFGAGTKLEIK 110
 DB 61 GIPARFSGSGGDTFTLNHPVEEEDAATYCOLCNEDEPTFGAGTKLEIK 111

RESULT 3

ID KV3Q_MOUSE STANDARD; PRT; 111 AA.
 AC P01667;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region PC 6308.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 diversity.";
 RL Nature 276:785-790(1978).
 DR HSSP; P80362; IWL.
 DR InterPro; IPR007110; Ig-Like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS0835; IG_LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 111
 FT DISULFID 23 92
 FT NON TER 111 111
 SQ SEQUENCE 111 AA; 12071 MW; 7A4ADE4D6C256D29 CRC64;

Query Match 89.9%; Score 523.5; DB 1; Length 111;

Best Local Similarity 91.9%; Pred. No. 1.8e-45;

Matches 102; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSDYDGDSYM-WYQKPGQPPKLLTYAASNLES 59
 DB 1 DIVLTQSPASLAVSLGORATISCKASQSDYDGDSYM-WYQKPGQPPKLLTYAASNLES 60
 QY 60 GIPARFSGSGGDTFTLNHPVEEEDAATYCOLCNEDEPTFGAGTKLEIK 110
 DB 61 GIPARFSGSGGDTFTLNHPVEEEDAATYCOLCNEDEPTFGAGTKLEIK 111

RESULT 4

ID KV3Q_MOUSE STANDARD; PRT; 111 AA.
 AC P01669;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region PC 7769.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 diversity.";
 RL Nature 276:785-790(1978).
 DR HSSP; P80362; IWL.
 DR InterPro; IPR007110; Ig-Like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS0835; IG_LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 111
 FT DISULFID 23 92
 FT NON TER 111 111
 SQ SEQUENCE 111 AA; 12011 MW; 6FAA345279356829 CRC64;

Query Match

Best Local Similarity 91.0%; Score 520.5; DB 1; Length 111;

Matches 101; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSDYDGDSYM-WYQKPGQPPKLLTYAASNLES 59
 DB 1 DIVLTQSPASLAVSLGORATISCKASQSDYDGDSYM-WYQKPGQPPKLLTYAASNLES 60

```

QY 60 GIPARFSGSGGDTFTLNHPVEEDAATYQCNCNEDPTFGAGTKLEIK 110
DB 61 GIPARFSGSGGDTFTLNHPVEEDAATYQCNCNEDPTFGAGTKLEIK 111

RESULT 5
KV3L_MOUSE STANDARD; PRT; 110 AA.
AC P01668;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-III region FC 7210.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR PIR; D01937; KVM510.
DR HSP; P01679; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 100
FT DOMAIN 101 110
FT DISULFID 23 92
FT NON_TER 110 110
SQ SEQUENCE 110 AA; 11950 MW; 69F1A5CE886B1249 CRC64;

Query Match 86.8%; Score 505; DB 1; Length 110;
Best Local Similarity 90.1%; Pred. No. 1.2e-43;
Matches 100; Conservative 4; Mismatches 5; Indels 2; Gaps 2;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSDYDGDYSN-WYQKPGQPPKLLTYAASNLES 59
DB 1 DIVLTQSPASLAVSLGQRATISCKASQSDYDGDYSNWNWYQKPGQPPKLLTYAASNLES 60

RESULT 6
KV3L_MOUSE STANDARD; PRT; 111 AA.
AC P01664;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-III region CBPC 101.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79012520; PubMed=99744;

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RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity; multiple genes encode structurally
related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
CC !- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A01936; KVM5C1.
DR HSP; P0362; 1WTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11964 MW; E2B1AD98AD965962 CRC64;

Query Match 86.5%; Score 503.5; DB 1; Length 111;
Best Local Similarity 89.2%; Pred. No. 1.8e-43;
Matches 99; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSDYDGDYSN-WYQKPGQPPKLLTYAASNLES 59
DB 1 DIVLTQSPASLAVSLGQRATISCKASQSDYDGDYSNWNWYQKPGQPPKLLTYAASNLES 60

QY 60 GIPARFSGSGGDTFTLNHPVEEDAATYQCNCNEDPTFGAGTKLEIK 110
DB 61 GIPARFSGSGGDTFTLNHPVEEDAATYQCNCNEDPTFGAGTKLEIK 111

RESULT 7
KV3L_MOUSE STANDARD; PRT; 111 AA.
AC P01671;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-III region FC 7175.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR PIR; B01938; KVM575.
DR HSP; P01679; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
SQ SEQUENCE 102 111

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FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111
SQ SEQUENCE 111 AA; 12010 MW; F041E89AA7858523 CRC64;

Query Match 81.4%; Score 473.5; DB 1; Length 111;
Best Local Similarity 85.6%; Pred. No. 1.7e-40;
Matches 95; Conservative 3; Mismatches 12; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSDYDGDSDM-WYQKPGQPPKLLTYAASNL 59
Db 1 DIVLTQSPASLAVSLGQRATISCRASKSVSTSGSYMHYQKPGQPPKLLTYLASNL 60

QY 60 GIPARFSGSGGTDFTLNHPVEEDAAATYYCQNCNEDPPTFGAGTKLEK 110
Db 61 GVPARFSGSGGTDFTLNHPVEEDAAATYYCQHSRELPLTFGAGTKLEK 111

RESULT 8
KV3T MOUSE
ID KV3T_MOUSE STANDARD; PRT; 111 AA.
AC P01670;

DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7940.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR HSP; P80362; IWL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 39 53 FRAMEWORK-2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 61 92 FRAMEWORK-3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111
SQ SEQUENCE 111 AA; 12038 MW; E8A82306084352E CRC64;

Query Match 80.8%; Score 470.5; DB 1; Length 111;
Best Local Similarity 83.8%; Pred. No. 3.4e-40;
Matches 93; Conservative 4; Mismatches 13; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSDYDGDSDM-WYQKPGQPPKLLTYAASNL 59
Db 1 DIVLTQSPASLAVSLGQRATISCRASKSVSTSGSYMHYQKPGQPPKLLTYLASNL 60

QY 60 GIPARFSGSGGTDFTLNHPVEEDAAATYYCQNCNEDPPTFGAGTKLEK 110
Db 61 GVPARFSGSGGTDFTLNHPVEEDAAATYYCQHSRELPLTFGAGTKLEK 111

RESULT 9
KV3R MOUSE
ID KV3R_MOUSE STANDARD; PRT; 111 AA.
AC P01670;
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DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 6684.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR HSP; P80362; IWL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 39 53 FRAMEWORK-2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 61 92 FRAMEWORK-3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111
SQ SEQUENCE 111 AA; 12039 MW; 1E46988341858526 CRC64;

Query Match 80.5%; Score 468.5; DB 1; Length 111;
Best Local Similarity 83.8%; Pred. No. 5.4e-40;
Matches 93; Conservative 4; Mismatches 13; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSDYDGDSDM-WYQKPGQPPKLLTYAASNL 59
Db 1 DIVLTQSPASLAVSLGQRATISCRASKSVSTSGSYMHYQKPGQPPKLLTYLASNL 60

QY 60 GIPARFSGSGGTDFTLNHPVEEDAAATYYCQNCNEDPPTFGAGTKLEK 110
Db 61 GVPARFSGSGGTDFTLNHPVEEDAAATYYCQHSRELPLTFGAGTKLEK 111

RESULT 10
KV3H MOUSE
ID KV3H_MOUSE STANDARD; PRT; 111 AA.
AC P01650;

DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 3741/TEPC 111.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (PC 3741).
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
RN [2]
RP SEQUENCE (TEPC 111).
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
related mouse kappa variable regions.";
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RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917 (1978).
CC -1- MISCELLANEOUS: THE PC 3741 AND TPC 111 SEQUENCES ARE IDENTICAL.
DR PIR; A93204; KWS37.
DR HSP; P01679; 2PBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON TER 111 111
SQ SEQUENCE 111 AA; 12099 MW; EC46C9D259213BE4 CRC64;

Query Match 78.3%; Score 455.5; DB 1; Length 111;
Best Local Similarity 81.1%; Pred. No. 1.1e-38;
Matches 90; Conservative 7; Mismatches 13; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSYDYDGDSYM-WYQOKPGOPPKLLTYAASNL 59
DB 1 DIVLTQSPASLAVSLGORATISCRASESDVSNGSFHMYQKPGOPPKLLTYASNL 60
QY 60 GIPARFSGSGGDTFTLNHPVEEADAATYVYCOLCNEDEPTFGAGTKLEK 110
DB 61 GIPARFSGSGRDTFTLNHPVEADDAATYVYCOQNEDEPTFGAGTKLEK 111

RESULT 11
KV3K MOUSE STANDARD; PRT; 111 AA.
ID KV3K MOUSE STANDARD; PRT; 111 AA.
AC P01663;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 4050.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity."
EL Nature 276:785-790 (1978).
CC -1- MISCELLANEOUS: THE PC 4285 AND PC 4039 SEQUENCES ARE IDENTICAL.
DR PIR; A01939; KWS85.
DR HSP; P01679; 2PBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON TER 111 111
SQ SEQUENCE 111 AA; 11986 MW; BF38CS9AA7858467 CRC64;

Query Match 78.1%; Score 454.5; DB 1; Length 111;
Best Local Similarity 82.9%; Pred. No. 1.3e-38;
Matches 92; Conservative 4; Mismatches 14; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSYDYDGDSYM-WYQOKPGOPPKLLTYAASNL 59
DB 1 DIVLTQSPASLAVSLGORATISCRASESDVSNGSFHMYQKPGOPPKLLTYASNL 60
QY 60 GIPARFSGSGGDTFTLNHPVEEADAATYVYCOLCNEDEPTFGAGTKLEK 110
DB 61 GIPARFSGSGRDTFTLNHPVEADDAATYVYCOQNEDEPTFGAGTKLEK 111

RESULT 13
KV3J MOUSE STANDARD; PRT; 111 AA.
ID KV3J MOUSE STANDARD; PRT; 111 AA.
AC P01662;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

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DR Pfam; PF00047; ig; 1.
 DR SMART; SMC0406; IGV; 1.
 DR PROSITE; PSS0835; IG LIKE; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 111
 FT DISULFID 23 92
 FT NON TER 111 111
 SQ SEQUENCE 111 AA; 11904 MW; 4FE7ABCGDFDF0FC125 CRC64;
 Query Match 74.8%; Score 435.5; DB 1; Length 111;
 Best Local Similarity 76.8%; Pred. No. 1e-36;
 Matches 85; Conservative 10; Mismatches 15; Indels 1; Gaps 1;
 Qy 1 DIVLTNSPASLAVSLGQRATISCKASQSYVDYDGDYSY-WYQKPGQPPKLLTYAASNLES 59
 Db 1 DIVLTQSPASLAVSLGQRATISCRASESVDSNGISPMWVQKPGQPPKLLIYAASNOGS 60
 Qy 60 GIPARFSGSGCTDFTLNHPVEEDAAATYQCLCNEDPPTGAGTKLEK 110
 Db 61 GVPARFSGSGCTDFTLNHPVEEDPTAMVFCQSQKEVPTFGGTKLEIK 111

Search completed: January 14, 2004, 19:11:51
 Job time : 10 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 14, 2004, 18:55:07 ; Search time 33.3333 Seconds
(without alignments)
851.574 Million cell updates/sec

Title: US-09-759-112A-24
Perfect score: 582
Sequence: 1 DIVLNSPASLAVSLGQRAT.....COLCNEDEPTFGAGTKLELK 110

Scoring table: BLOSUM62

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTEMBL_23.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phage.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rviro.*

16: sp_bacteriap.*

17: sp_archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	467.5	80.3	111	11 Q920E9	Q920E9 mus musculus
2	413.5	71.0	103	11 Q9JL80	Q9JL80 mus musculus
3	352.5	60.6	108	4 Q9UL70	Q9UL70 homo sapien
4	348.5	59.9	108	4 Q9UL79	Q9UL79 homo sapien
5	346	59.5	109	4 Q9UL78	Q9UL78 homo sapien
6	342	58.8	238	11 Q9VCL6	Q9VCL6 mus musculus
7	341.5	58.7	108	4 Q9UL77	Q9UL77 homo sapien
8	341.5	58.7	234	4 Q9NEK1	Q9NEK1 homo sapien
9	341	58.6	107	4 Q96SA9	Q96SA9 homo sapien
10	340	58.4	112	11 Q8K1F2	Q8K1F2 mus musculus
11	338.5	58.2	108	4 Q9UL83	Q9UL83 homo sapien
12	335	57.6	109	4 Q9UL85	Q9UL85 homo sapien
13	335	57.6	112	11 Q8K1F3	Q8K1F3 mus musculus
14	334	57.4	238	11 Q99M37	Q99M37 mus musculus
15	334	57.4	239	4 Q8TCD0	Q8TCD0 homo sapien
16	330	56.7	114	11 Q8K1F1	Q8K1F1 mus musculus

17	327	56.2	239	11 Q8VC55	Q8VC55 mus musculus
18	325.5	55.9	114	4 Q9UL80	Q9UL80 homo sapien
19	325	55.8	107	4 Q9UL81	Q9UL81 homo sapien
20	324	55.7	239	4 Q8NEK0	Q8NEK0 homo sapien
21	321.5	55.2	108	11 Q8VIJ0	Q8VIJ0 mus musculus
22	314	54.0	106	5 Q9U410	Q9U410 schistosoma
23	313.5	53.9	214	11 Q9RIAS	Q9RIAS mus musculus
24	312	53.6	239	11 Q8K0F8	Q8K0F8 mus musculus
25	311	53.4	109	4 Q9UL86	Q9UL86 homo sapien
26	311	53.4	112	11 Q8K1F0	Q8K1F0 mus musculus
27	309.5	53.2	107	11 Q9RZ9	Q9RZ9 mus musculus
28	308	52.9	134	11 Q8VDD0	Q8VDD0 mus musculus
29	306.5	52.7	234	11 Q9LWF8	Q9LWF8 mus musculus
30	305.5	52.5	234	11 Q8R062	Q8R062 mus musculus
31	305	52.4	104	11 Q9UL82	Q9UL82 mus musculus
32	305	52.4	235	11 Q9LW12	Q9LW12 mus musculus
33	304.5	52.3	218	11 Q925S1	Q925S1 mus musculus
34	301.5	51.8	99	11 Q9JL74	Q9JL74 mus musculus
35	299.5	51.5	233	11 Q9LWS9	Q9LWS9 mus musculus
36	294.5	50.6	234	11 Q8VCP0	Q8VCP0 mus musculus
37	293.5	50.4	298	11 Q9QYF0	Q9QYF0 mus musculus
38	291.5	50.1	109	11 Q920E6	Q920E6 mus musculus
39	289.5	49.7	107	11 Q9UL84	Q9UL84 mus musculus
40	288.5	49.6	116	4 Q96PF6	Q96PF6 homo sapien
41	288.5	49.6	234	11 Q8R028	Q8R028 mus musculus
42	286.5	49.2	57	11 Q9UL76	Q9UL76 mus musculus
43	283.5	48.7	101	11 Q9UL78	Q9UL78 mus musculus
44	280	48.1	148	11 Q8K122	Q8K122 mus musculus
45	279.5	48.0	109	6 Q9NOW5	Q9NOW5 oryctolagus

ALIGNMENTS

RESULT 1
Q920E9 PRELIMINARY; PRT; 111 AA.
AC Q920E9: 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Pterin-mimicking anti-idiotope kappa chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed in Mammalian Cells."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF079355; AAL09419.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1 111
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12046 MW; 1E469898AA6858526 CRC64;

Query Match 80.3%; Score 467.5; DB 11; Length 111;
Best Local Similarity 83.8%; Pred. No. 1.5e-43;
Matches 93; Conservative 4; Mismatches 13; Indels 1; Gaps 1;
QY 1 DIVLNSPASLAVSLGQRATISCKASQSYVDYDGSYM-WYQKQPQPKLLTYAASNLES 59
Db 1 DIVLTQSPASLAVSLGQRATISCKASQSYVDYDGSYM-WYQKQPQPKLLTYAASNLES 60
QY 60 GIPARFSGSGSTDFTLNHPVEEEDATYYCOLCNEDEPTFGAGTKLELK 110


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AC Q9UL78;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035036; AAD56272.1; -.
DR HSP; P80362; IWL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 109
FT NON_TER 109
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match
Best Local Similarity 59.5%; Score 346; DB 4; Length 109;
Matches 69; Conservative 14; Mismatches 24; Indels 4; Gaps 2;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSYVDYDGSYM-WYQKPGQPPKLLTYAASNLE 59
DB 1 EIVLTQSPGTLSPGERATLSCRAQSV-SSSYLAWYQKPGAPRLIYGASRRAT 57
QY 60 GIPARFSGSGGTDFTLNIHPVEEDAAATYQCLNEDPPTFGAGTKLEIK 110
DB 58 GIPDRFSGSGGTDFTLTISRLEPEDCAVYQCYGSSPLTFGGTKVRIK 108

RESULT 6
Q8VC16 PRELIMINARY; PRT; 238 AA.
AC Q8VC16;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 26.2 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX Tissue=Colon;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019760; AAH19760.1; -.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS0290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;

Query Match
Best Local Similarity 58.8%; Score 342; DB 11; Length 238;
Matches 68; Conservative 14; Mismatches 28; Indels 2; Gaps 2;

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QY 1 DIVLTNSPASLAVSLGQRATISCKASQSYVDYDGSYM-WYQKPGQPPKLLTYAASNLE 58
DB 20 DVMTQIFLSLPVSLGDSISCRSSQSLVHNGTYLHWYLRQPGQSPKLLIYKVSNR 79
QY 59 SCIPARFSGSGGTDFTLNIHPVEEDAAATYQCLNEDPPTFGAGTKLEIK 110
DB 80 SGVPDRFSGSGGTDFTLKISRVEAEDLGVVFCQSQTHTVPTFGGTYKLEIK 131

RESULT 7
Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match
Best Local Similarity 58.7%; Score 341.5; DB 4; Length 108;
Matches 67; Conservative 17; Mismatches 22; Indels 5; Gaps 2;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSYVDYDGSYM-WYQKPGQPPKLLTYAASNLE 59
DB 1 DIQWTQSPSSLSASVGDRTVITCRASQSI-SSYLWYQKPGKAPNLLIYAASLS 56
QY 60 GIPARFSGSGGTDFTLNIHPVEEDAAATYQCLNEDPPTFGAGTKLEIK 110
DB 57 GVPSRFSGSGGTDFTLTITSLQPEDFATYQCYQSYSTSTWTGEGTKVRIK 107

RESULT 8
Q8NEK1 PRELIMINARY; PRT; 234 AA.
AC Q8NEK1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Tissue=Lung;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC030813; AAH30813.1; -.

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SQ SEQUENCE 108 AA; 11834 MW; 3F9C5A92EBA96EEA CRC64;
Query Match
Best Local Similarity 58.2%; Score 338.5; DB 4; Length 108;
Matches 67; Conservative 16; Mismatches 24; Indels 3; Gaps 1;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSDYDGDSDYMWYQKQPPKLLTYAASNLESG 60
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
1 EIVMTQSPATLSVSPGERATLSQASQSV---SSNLAWYQKQPPKLLTYCASTRATG 57

QY 61 IPARFSGSGGTDFTLNIHPVEEEDATYYCQLCNEDPPTFGAGTKLELK 110
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
58 IPARFSGSGGTDFTLNISLQEDFAVYVCQYNNWPFPGGTGKVDIK 107

RESULT 12
Q9UL85 PRELIMINARY; PRT; 109 AA.
AC Q9UL85
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin kappa chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berner S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035029; AAD56265.1; -.
DR HSP; P80362; IWL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11761 MW; FB1B43B7C7AFACCC CRC64;

Query Match
Best Local Similarity 57.6%; Score 335; DB 4; Length 109;
Matches 67; Conservative 16; Mismatches 24; Indels 4; Gaps 2;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSDYDGDSDYMWYQKQPPKLLTYAASNLESG 60
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
1 EIVMTQSPATLSVSPGERATLSQASQSV---SSNLAWYQKQPPKLLTYCASTRATG 57

QY 61 IPARFSGSGGTDFTLNIHPVEEEDATYYCQLCNEDPPTFGAGTKLELK 110
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
58 IPARFSGSGGTDFTLNISLQEDFAVYVCQYNNWPFPGGTGKVDIK 108

RESULT 13
Q8K1F3 PRELIMINARY; PRT; 112 AA.
AC Q8K1F3
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Anti-VIPase light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/C; TISSUE=Hyperimmunized spleen;
RA Zhou Y.-X., Taguchi H., Planque S., Karie S., Nishiyama Y., Paul S.;
RT Innate proteolytic antibodies: Failed D-Vipase response to the D-
RL entanioner of VIP and identification of L-Vipase VL domains."
DR EMBL; AF516282; AAM64200.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 112
SQ SEQUENCE 112 AA; 12017 MW; 22DD75B5414CDB18 CRC64;

Query Match
Best Local Similarity 57.6%; Score 335; DB 11; Length 112;
Matches 67; Conservative 10; Mismatches 29; Indels 4; Gaps 1;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSDYDGDSDYMWYQKQPPKLLTYAASNLESG 60
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
1 DIVLTQSPAINASPGKVTITSCSASSVS---MYWYQKQPPKLLTYRTSNLASG 56

QY 61 IPARFSGSGGTDFTLNIHPVEEEDATYYCQLCNEDPPTFGAGTKLELK 110
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
57 VPARFSGSGGTSLTISSEWEADATYYCQVHSYPTIFGGTKLEIK 106

RESULT 14
Q99M37 PRELIMINARY; PRT; 238 AA.
AC Q99M37
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical 26.3 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002035; AAB02035.1; -.
DR HSP; P01679; 2PB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

Query Match
Best Local Similarity 57.4%; Score 334; DB 11; Length 238;
Matches 67; Conservative 17; Mismatches 26; Indels 2; Gaps 2;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSDYDGDSDYMWYQKQPPKLLTYAASNLE 58
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
20 DVMTQTPUSLPVSLGQDQASISCRSSQSIHNGNTYLEWYKQPPKLLTYKVSNR 79

QY 59 SGIPARFSGSGGTDFTLNIHPVEEEDATYYCQLCNEDPPTFGAGTKLELK 110
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
80 SGVPDRFSGSGGTDFTLKISRVEADLGYVYCFQGSHPVTFGSGTKLEIK 131
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OM protein - protein search, using sw model

Run on: January 14, 2004, 19:10:12 ; Search time 13.8095 Seconds
(without alignments)
337.028 Million cell updates/sec

Title: US-09-759-112A-24
Perfect score: 582
Sequence: 1 DIVLTNSPASLAVSLQCRAT.....COLCNEBPPTFGAGTKLELK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/prodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/prodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/prodata/2/iaa/6C_COMB.pep.*
6: /cgn2_6/prodata/2/iaa/6D_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	537.5	92.4	132	2	US-08-483-636-2
2	537.5	92.4	132	2	US-08-483-632-2
3	519.5	89.3	111	1	US-08-491-845-8
4	516.5	88.7	131	3	US-08-579-378A-14
5	503.5	86.5	106	3	US-08-466-151-6
6	503.5	86.5	106	4	US-08-466-163B-6
7	491.5	84.5	111	3	US-08-466-151-2
8	491.5	84.5	111	4	US-08-466-163B-2
9	490.5	84.3	120	1	US-08-111-080-24
10	490.5	84.3	120	1	US-08-211-980-24
11	490.5	84.3	120	5	PCT-US93-07967-24
12	485.5	83.4	111	3	US-08-887-352B-5
13	485.5	83.4	111	3	US-09-109-207C-5
14	485.5	83.4	111	3	US-09-296-005-5
15	469.5	80.7	131	2	US-08-483-636-58
16	469.5	80.7	131	2	US-08-483-632-58
17	465.5	80.0	131	1	US-08-137-117D-33
18	465.5	80.0	131	2	US-08-436-717-33
19	463.5	79.6	131	2	US-08-483-636-14
20	463.5	79.6	131	2	US-08-483-632-14
21	460.5	79.1	131	1	US-08-137-117D-25
22	460.5	79.1	131	2	US-08-436-717-25
23	453.5	77.9	111	1	US-08-621-751A-10
24	453.5	77.9	111	1	US-08-275-053-11
25	453.5	77.9	121	1	US-08-111-080-22
26	453.5	77.9	121	1	US-08-211-980-22
27	453.5	77.9	121	5	PCT-US93-07967-22

28	449.5	77.2	111	2	US-08-483-636-73	Sequence 73, Appl
29	449.5	77.2	111	2	US-08-483-632-73	Sequence 73, Appl
30	448.5	77.1	129	4	US-09-556-605-2	Sequence 2, Appl
31	447	76.8	151	4	US-09-318-786-33	Sequence 33, Appl
32	446.5	76.7	120	1	US-08-111-080-26	Sequence 26, Appl
33	446.5	76.7	120	1	US-08-211-980-26	Sequence 26, Appl
34	446.5	76.7	120	5	PCT-US93-07967-26	Sequence 26, Appl
35	444.5	76.4	111	1	US-08-207-169A-4	Sequence 4, Appl
36	444.5	76.4	121	1	US-08-111-980-18	Sequence 18, Appl
37	444.5	76.4	121	1	US-08-211-980-18	Sequence 18, Appl
38	444.5	76.4	121	5	PCT-US93-07111-17	Sequence 17, Appl
39	444.5	76.4	121	5	PCT-US93-07967-18	Sequence 18, Appl
40	444	76.3	110	1	US-08-017-570-2	Sequence 2, Appl
41	444	76.3	110	1	US-08-471-426-2	Sequence 2, Appl
42	444	76.3	110	4	US-09-672-609-13	Sequence 13, Appl
43	444	76.3	110	4	US-09-025-403A-13	Sequence 13, Appl
44	444	76.3	110	5	PCT-US94-01709-2	Sequence 2, Appl
45	439.5	75.5	132	2	US-08-379-057-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-08-483-636-2
; Sequence 2, Application US/08483636
; Patent No. 5914110
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,636
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-483-636-2

Query Match 92.4%; Score 537.5; DB 2; Length 132;
Best Local Similarity 93.7%; Pred. No. 2.2e-49;
Matches 104; Conservative 1; Mismatches 5; Indels 1; Gaps 1;
QY 1 DIVLTNSPASLAVSLGQRATISCKASQSDVDYDGDSYM-WYQKPGQPPKLLTYAASNLES 59
DB 21 DIVLTQSPASLAVSLGQRATISCKASQSDVDYDGDSYM-WYQKPGQPPKLLTYAASNLES 80
QY 60 GIPARFSGSGGTDTFLNIHPVEEDAATYYCOLCNEDEPTFGAGTKLEK 110
DB 81 GIPARFSGSGGTDTFLNIHPVEEDAATYYCQSNEDPTFGGTKLEIK 131

RESULT 2

US-08-483-632-2
; Sequence 2, Application US/08483632
; Patent No. 5928904
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,632
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 132 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-483-632-2

Query Match 92.4%; Score 537.5; DB 2; Length 132;
Best Local Similarity 93.7%; Pred. No. 2.2e-49;
Matches 104; Conservative 1; Mismatches 5; Indels 1; Gaps 1;
QY 1 DIVLTNSPASLAVSLGQRATISCKASQSDVDYDGDSYM-WYQKPGQPPKLLTYAASNLES 59

DB 21 DIVLTQSPASLAVSLGQRATISCKASQSDVDYDGDSYM-WYQKPGQPPKLLTYAASNLES 80
QY 60 GIPARFSGSGGTDTFLNIHPVEEDAATYYCOLCNEDEPTFGAGTKLEK 110
DB 81 GIPARFSGSGGTDTFLNIHPVEEDAATYYCQSNEDPTFGGTKLEIK 131

RESULT 3

US-08-491-845-8
; Sequence 8, Application US/08491845
; Patent No. 5773247
; GENERAL INFORMATION:
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: EDA, Yasuyuki
; APPLICANT: SHIOSAKI, Kouichi
; APPLICANT: OSATOMI, Kiyoshi
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: RECOMBINANT ANTI-HIV ANTIBODY AND
; TITLE OF INVENTION: PROCESS FOR PREPARING THE SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/491,845
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00039
; FILING DATE: 14-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: MAEDA=5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-491-845-8

Query Match 89.3%; Score 519.5; DB 1; Length 111;
Best Local Similarity 91.9%; Pred. No. 1.4e-47;
Matches 102; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

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DB 1 DIVLTQSPASLAVSLGQRATISCKASQSDVDYDGDSYM-WYQKPGQPPKLLTYAASNLES 60
QY 60 GIPARFSGSGGTDTFLNIHPVEEDAATYYCOLCNEDEPTFGAGTKLEK 110
DB 61 GIPARFSGSGGTDTFLNIHPVEEDAATYYCQSNEDPTFGGTKLEIK 111

RESULT 4

US-08-579-378A-14
; Sequence 14, Application US/08579378A
; Patent No. 6210671
; GENERAL INFORMATION:

APPLICANT: Co, Man Sung
TITLE OF INVENTION: Humanized Antibodies Reactive with
L-Selection
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/579,378A
FILING DATE: 27-DEC-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/160,074
FILING DATE: 30-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,946
FILING DATE: 01-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95112895.8
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95114696.8
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschultz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 11823-002220
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-579-378A-14

Query Match 88.7%; Score 516.5; DB 3; Length 131;
Best Local Similarity 90.1%; Pred. No. 3.5e-47;
Matches 100; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSVYDGDYSY-WYQKQGPQPKLLTYAASNLES 59
Db 21 DIVLTQSPASLSVSLGERASISCKASQSVYDGDYSYMWYQKQGPQPKLLTYAASNLES 80
QY 60 GIPARFSGSGGTDFTLNHPVEEEDAATYYCQLCNEDPPTFGAGTKLEIK 110
Db 81 GIPARFSGSGGTDFTLNHPVEEEDAATYYCQNSNEDPPTFGGTTKLEIK 131

RESULT 5
US-08-466-151-6
Sequence 6, Application US/08466151
Patent No. 6037453
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco

STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,151
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/466163
FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/405617
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/185899
FILING DATE: 26-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/879495
FILING DATE: 07-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744768
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P0718P2C1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-466-151-6

Query Match 86.5%; Score 503.5; DB 3; Length 106;
Best Local Similarity 93.4%; Pred. No. 6.4e-46;
Matches 99; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSVYDGDYSY-WYQKQGPQPKLLTYAASNLES 59
Db 1 DIVLTQSPASLAVSLGQRATISCKASQSVYDGDYSYMWYQKQGPQPKLLTYAASNLES 60
QY 60 GIPARFSGSGGTDFTLNHPVEEEDAATYYCQLCNEDPPTFGAGT 105
Db 61 GIPARFSGSGGTDFTLNHPVEEEDAATYYCQNSNEDPPTFGAGT 106

RESULT 6
US-08-466-163B-6
Sequence 6, Application US/08466163B
Patent No. 6328509
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: P0718P2C1D1
CURRENT APPLICATION NUMBER: US/08/466,163B
CURRENT FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR FILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1992-05-07
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 64

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; SEQ ID NO 6
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-466-163B-6

Query Match      86.5%; Score 503.5; DB 4; Length 106;
Best Local Similarity 93.4%; Pred. No. 6.4e-46;
Matches 99; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

Qy 1 DIVLTNSPASLAVSLGORATISCKASQSDYDGDSTM-WYQKPGOPPKLLTYAASNLES 59
Db 1 DIQLTSPASLAVSLGORATISCKASQSDYDGDSTMWYQKPGOPPKLLTYAASNLES 60

Qy 60 GIPARFSGSGGTDFTLNHPVEEEDAATYYCOLNEDPPTFGAGT 105
Db 61 GIPARFSGSGGTDFTLNHPVEEEDAATYYCQSNEDPPTFGACT 106

RESULT 7
US-08-466-151-2
; Sequence 2, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; APPLICATION DATA:
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Syvoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P07182C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-466-151-2

Query Match      84.5%; Score 491.5; DB 3; Length 111;

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Best Local Similarity 88.3%; Pred. No. 1.2e-44;
Matches 98; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

Qy 1 DIVLTNSPASLAVSLGORATISCKASQSDYDGDSTM-WYQKPGOPPKLLTYAASNLES 59
Db 1 DIVLTQSPASLAVSLGORATISCKASQSDYDGDSTMWYQKPGOPPKLLTYAASYLGS 60

Qy 60 GIPARFSGSGGTDFTLNHPVEEEDAATYYCOLNEDPPTFGAGTKLEIK 110
Db 61 EIPARFSGSGGTDFTLNHPVEEEDAATFYCQSHEDPPTFGAGTKLEIK 111

RESULT 8
US-08-466-163B-2
; Sequence 2, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Immunoglobulin Variants
; FILE REFERENCE: P0718P2C1D1
; CURRENT APPLICATION NUMBER: US/08/466,163B
; CURRENT FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 2
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-466-163B-2

Query Match      84.5%; Score 491.5; DB 4; Length 111;
Best Local Similarity 88.3%; Pred. No. 1.2e-44;
Matches 98; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

Qy 1 DIVLTNSPASLAVSLGORATISCKASQSDYDGDSTM-WYQKPGOPPKLLTYAASNLES 59
Db 1 DIVLTQSPASLAVSLGORATISCKASQSDYDGDSTMWYQKPGOPPKLLTYAASYLGS 60

Qy 60 GIPARFSGSGGTDFTLNHPVEEEDAATYYCOLNEDPPTFGAGTKLEIK 110
Db 61 EIPARFSGSGGTDFTLNHPVEEEDAATFYCQSHEDPPTFGAGTKLEIK 111

RESULT 9
US-08-111-080-24
; Sequence 24, Application 08/111080
; Patent No. 5558865
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; TITLE OF INVENTION: HIV Immunotherapeutics
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: 08/111,080
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/748,562
; FILING DATE: 22-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/07111
; FILING DATE: 24-AUG-1992
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,457
; FILING DATE: 22-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 31629
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-111-080-24

Query Match      84.3%; Score 490.5; DB 1; Length 120;
Best Local Similarity 87.3%; Pred. No. 1.7e-44;
Matches 96; Conservative 3; Mismatches 10; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSDYDGDSDYK-WYQKPGOPPKLLTYAASNLES 59
Db 1 DIVLTQSPASLAVSLGORATISCKASQSDYDGDSDYK-WYQKPGOPPKLLTYAASNLES 60
QY 60 GIPARFSGSGGDTFTLNHPVEEEDATYYQQLCNEEDPTFGAGTKLEL 109
Db 61 GIPARFYGSGGDTFTNTIHPVEEEDATYYQQLCNEEDPTFGAGTKLEI 110

RESULT 10
US-08-211-980-24
; Sequence 24, Application US/08211980
; Patent No. 5665569
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; TITLE OF INVENTION: HIV Immunotherapeutics
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/211,980
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/07111
; FILING DATE: 24-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,457
; FILING DATE: 22-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 31629
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-211-980-24
```

```

; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 31629
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-211-980-24

Query Match      84.3%; Score 490.5; DB 1; Length 120;
Best Local Similarity 87.3%; Pred. No. 1.7e-44;
Matches 96; Conservative 3; Mismatches 10; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSDYDGDSDYK-WYQKPGOPPKLLTYAASNLES 59
Db 1 DIVLTQSPASLAVSLGORATISCKASQSDYDGDSDYK-WYQKPGOPPKLLTYAASNLES 60
QY 60 GIPARFSGSGGDTFTLNHPVEEEDATYYQQLCNEEDPTFGAGTKLEL 109
Db 61 GIPARFYGSGGDTFTNTIHPVEEEDATYYQQLCNEEDPTFGAGTKLEI 110

RESULT 11
PCT-US93-07967-24
; Sequence 24, Application PC/TUS9307967
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; TITLE OF INVENTION: HIV Immunotherapeutics
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07967
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/07111
; FILING DATE: 24-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,457
; FILING DATE: 22-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 31629
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US93-07967-24
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Query Match      84.3%; Score 490.5; DB 5; Length 120;
Best Local Similarity 87.3%; Pred. No. 1.7e-44;
Matches 96; Conservative 3; Mismatches 10; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSYDYGDSYM-WYQKPGQPPKLLTYAASNL 59
Db 1 DIVLTQSPASLAVSLGQRATISCKASQSYDYGDSYM-WYQKPGQPPKLLTYAASNL 60

QY 60 GIPARFSGSGTGDTFTLNHPVEEEDAATYCOLCNEDEPTFGAGTKLEL 109
Db 61 GIPARFYGSGSGTGDTFTLNHPVEEEDAATYCOLCNEDEPTFGAGTKLEI 110

RESULT 12
US-08-887-352B-5
; Sequence 5, Application US/08897352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Sycboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-5

Query Match      83.4%; Score 485.5; DB 2; Length 111;
Best Local Similarity 87.4%; Pred. No. 5.3e-44;
Matches 97; Conservative 3; Mismatches 10; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSYDYGDSYM-WYQKPGQPPKLLTYAASNL 59
Db 1 DIVLTQSPASLAVSLGQRATISCKASQSYDYGDSYM-WYQKPGQPPKLLTYAASYL 60

QY 60 GIPARFSGSGTGDTFTLNHPVEEEDAATYCOLCNEDEPTFGAGTKLEL 110
Db 61 EIPARFSGSGTGDTFTLNHPVEEEDAATFYCQSHEDPYTFGAGTKLEIK 111

RESULT 13
US-09-109-207C-5
; Sequence 5, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
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FILE REFERENCE: P1123R1
CURRENT APPLICATION NUMBER: US/09/109,207C
CURRENT FILING DATE: 1998-08-30
PRIOR APPLICATION NUMBER: US 60/051,554
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 5
LENGTH: 111
TYPE: PRT
ORGANISM: Mus musculus
US-09-109-207C-5

Query Match      83.4%; Score 485.5; DB 3; Length 111;
Best Local Similarity 87.4%; Pred. No. 5.3e-44;
Matches 97; Conservative 3; Mismatches 10; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSYDYGDSYM-WYQKPGQPPKLLTYAASNL 59
Db 1 DIVLTQSPASLAVSLGQRATISCKASQSYDYGDSYM-WYQKPGQPPKLLTYAASYL 60

QY 60 GIPARFSGSGTGDTFTLNHPVEEEDAATYCOLCNEDEPTFGAGTKLEL 110
Db 61 EIPARFSGSGTGDTFTLNHPVEEEDAATFYCQSHEDPYTFGAGTKLEIK 111

RESULT 14
US-09-296-005-5
; Sequence 5, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide:
; FILE REFERENCE: P1123C1r
; CURRENT APPLICATION NUMBER: US/09/296,005
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/887,352
; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 5
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-296-005-5

Query Match      83.4%; Score 485.5; DB 3; Length 111;
Best Local Similarity 87.4%; Pred. No. 5.3e-44;
Matches 97; Conservative 3; Mismatches 10; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSYDYGDSYM-WYQKPGQPPKLLTYAASNL 59
Db 1 DIVLTQSPASLAVSLGQRATISCKASQSYDYGDSYM-WYQKPGQPPKLLTYAASYL 60

QY 60 GIPARFSGSGTGDTFTLNHPVEEEDAATYCOLCNEDEPTFGAGTKLEL 110
Db 61 EIPARFSGSGTGDTFTLNHPVEEEDAATFYCQSHEDPYTFGAGTKLEIK 111

RESULT 15
US-08-483-636-58
; Sequence 58, Application US/08483636
; Patent No. 5914110
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
```

STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,636
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5030
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-636-58

Query Match 80.7%; Score 469.5; DB 2; Length 131;
Best Local Similarity 80.2%; Pred. No. 3.1e-42;
Matches 89; Conservative 8; Mismatches 13; Indels 1; Gaps 1;
QY 1 DIVLTNSPASLAVSLGRATISKASQSYVDYDGDSYM-WYQOKPGQPPKLLIYAASNL 59
Db 20 DIVMTQSPDLSAVSLGERATINCKASQSYVDYDGDSYMWYQOKPGQPPKLLIYAASNL 79
QY 60 GIPARFSGSGGTDFTLNIHPVEEDATYYCQLCNEDPPTFGAGTKLELK 110
Db 80 GVPDRFSGSGGTDFTLTISSLQAEDVAVYYCQSNEDPPTFGGKVEIK 130

Search completed: January 14, 2004, 19:14:24
Job time : 14.8095 secs

Result	No.	Query			DB	ID	Description
		Score	Match	Length			
1	582	100.0	110	11	US-09-759-112A-24	Sequence 24, Appl	
2	537.5	92.4	132	10	US-09-879-461-2	Sequence 2, Appl	
3	538.5	90.8	238	12	US-10-384-933-11	Sequence 11, Appl	
4	528.5	90.8	238	15	US-10-216-484-11	Sequence 11, Appl	
5	526.5	90.5	238	10	US-09-503-327A-4	Sequence 4, Appl	
6	505.5	86.9	112	15	US-10-194-975-115	Sequence 115, App	
7	503.5	86.5	106	9	US-09-802-077-6	Sequence 6, Appl	
8	503.5	86.5	106	9	US-09-802-066-6	Sequence 6, Appl	
9	503.5	86.5	106	11	US-09-925-179-6	Sequence 6, Appl	
10	491.5	84.5	111	9	US-09-802-077-2	Sequence 2, Appl	
11	491.5	84.5	111	9	US-09-802-096-2	Sequence 2, Appl	
12	491.5	84.5	111	11	US-09-925-179-2	Sequence 2, Appl	
13	490	84.2	112	12	US-10-160-506-81	Sequence 81, Appl	
14	487.5	83.8	238	12	US-10-384-933-54	Sequence 54, Appl	
15	487.5	83.8	238	15	US-10-216-484-54	Sequence 54, Appl	

```

; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; Gross, Mitchell S.
; Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: Corporate Intellectual Property, UW2220 - 709
; CITY: Swedeland Rd.
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/879,461
; FILING DATE: 12-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/612,929
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/136,783
; FILING DATE: 14-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FILE REFERENCE: 980126CIP/HG
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-879-461-2

Query Match          92.4%; Score 537.5; DB 10; Length 132;
Best Local Similarity 93.7%; Pred. No. 6.1e-45;
Matches 104; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

Qy 1 DIVLTNSPASLAVSLGORATISKASQSDVDYDGSYM-WYQQKPGPPKLLTYAASNLES 59
Db 21 DIVLTQSPASLAVSLGORATISKASQSDVDYDGSYMNWYQQKPGPPKLLIYAASNLES 80

Qy 60 GIPARFSGSGSGTDFTLNHPHVEEEDAAATYYCOLCNEDEPPTFGAGTKLEIK 110
Db 81 GIPARFSGSGSGTDFTLNHPHVEEEDAAATYYCQSNEDPPTFGGKLEIK 131

RESULT 3
US-10-384-933-11
; Sequence 11, Application US/10384933
; Publication No. US20030170817A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030170817A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/384,933
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/499,662

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; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 11
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-384-933-11

Query Match          90.8%; Score 528.5; DB 12; Length 238;
Best Local Similarity 92.8%; Pred. No. 8.8e-44;
Matches 103; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

Qy 1 DIVLTNSPASLAVSLGORATISKASQSDVDYDGSYM-WYQQKPGPPKLLTYAASNLES 59
Db 21 DIVLTQSPASLAVSLGORATISKASQSDVDYDGSYMNWYQQKPGPPKLLIYAASNLES 80

Qy 60 GIPARFSGSGSGTDFTLNHPHVEEEDAAATYYCOLCNEDEPPTFGAGTKLEIK 110
Db 81 GIPARFSGSGSGTDFTLNHPHVEEEDAAATYYCQSNEDPPTFGGKLEIK 131

RESULT 4
US-10-216-484-11
; Sequence 11, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030103976A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 11
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-216-484-11

Query Match          90.8%; Score 528.5; DB 15; Length 238;
Best Local Similarity 92.8%; Pred. No. 8.8e-44;
Matches 103; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

Qy 1 DIVLTNSPASLAVSLGORATISKASQSDVDYDGSYM-WYQQKPGPPKLLTYAASNLES 59
Db 21 DIVLTQSPASLAVSLGORATISKASQSDVDYDGSYMNWYQQKPGPPKLLIYAASNLES 80

Qy 60 GIPARFSGSGSGTDFTLNHPHVEEEDAAATYYCOLCNEDEPPTFGAGTKLEIK 110
Db 81 GIPARFSGSGSGTDFTLNHPHVEEEDAAATYYCQSNEDPPTFGGKLEIK 131

RESULT 5
US-09-903-327A-4
; Sequence 4, Application US/09903327A
; Patent No. US20020164333A1
; GENERAL INFORMATION:
; APPLICANT: Nemerow, Glen R.
; APPLICANT: Li, Eryuang
; TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGETED
; DELIVERY
; TITLE OF INVENTION: GENE
; FILE REFERENCE: 22908-1228
; CURRENT APPLICATION NUMBER: US/09/903,327A

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; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 09/613,017
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (0)...(0)
; OTHER INFORMATION: DAV-1 light chain, penton base monoclonal antibody
US-09-903-327A-4

Query Match
Best Local Similarity 90.5%; Score 526.5; DB 10; Length 238;
Matches 103; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSDYDGDSYM-WYQKPGQPPKLLTYAASNLES 59
Db 21 DIVLTQSPASLAVSLGORATISCKASQSDYDGDSTNNWYQKPGQPPKLLTYAASNLES 80
QY 60 GIPARFSGSGGTDFTLNHPVEEDAATYYCOLCNEDEPPTFGAGTKLEK 110
Db 81 GIPARFSGSGGTDFTLNHPVEEDAATYYCQQTNEDEPPTFGAGTKLEK 131

RESULT 6
US-10-194-975-115
; Sequence 115, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 115
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-194-975-115

Query Match
Best Local Similarity 86.9%; Score 505.5; DB 15; Length 112;
Matches 98; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSDYDGDSYM-WYQKPGQPPKLLTYAASNLES 59
Db 1 DIVLTQSPVSLAVSLGORATISCKASQSDYDGDSTNNWYQKPGQPPKLLTYVVSNLES 60
QY 60 GIPARFSGSGGTDFTLNHPVEEDAATYYCOLCNEDEPPTFGAGTKLEK 110
Db 61 GIPARFSGSGGTDFTLNHPVEEDAATYYCQQTNEDEPPTFGAGTKLEK 111

RESULT 7
US-09-802-077-6
; Sequence 6, Application US/09802077
; Patent No. US20010033842A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Paula M.
; APPLICANT: Jardieu, Leonard G.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
```

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; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 6
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-802-077-6

Query Match
Best Local Similarity 86.5%; Score 503.5; DB 9; Length 106;
Matches 99; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSDYDGDSYM-WYQKPGQPPKLLTYAASNLES 59
Db 1 DIQLTQSPASLAVSLGORATISCKASQSDYDGDSTNNWYQKPGQPPKLLTYAASNLES 60
QY 60 GIPARFSGSGGTDFTLNHPVEEDAATYYCOLCNEDEPPTFGAGT 105
Db 61 GIPARFSGSGGTDFTLNHPVEEDAATYYCQQTNEDEPPTFGAGT 106

RESULT 8
US-09-802-096-6
; Sequence 6, Application US/09802096
; Patent No. US20010038839A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Paula M.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P07182C3US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 6
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-802-096-6

Query Match
Best Local Similarity 86.5%; Score 503.5; DB 9; Length 106;
Matches 99; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSDYDGDSYM-WYQKPGQPPKLLTYAASNLES 59
Db 1 DIQLTQSPASLAVSLGORATISCKASQSDYDGDSTNNWYQKPGQPPKLLTYAASNLES 60
QY 60 GIPARFSGSGGTDFTLNHPVEEDAATYYCOLCNEDEPPTFGAGT 105
Db 61 GIPARFSGSGGTDFTLNHPVEEDAATYYCQQTNEDEPPTFGAGT 106

RESULT 9
US-09-925-179-6
; Sequence 6, Application US/09925179
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```

; Publication No. US20030044858A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-IGE Antibodies (as amended)
; FILE REFERENCE: P0718P2C1D1C1US
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 6
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-925-179-6

Query Match      86.5%; Score 503.5; DB 11; Length 106;
Best Local Similarity 93.4%; Pred. No. 9.9e-42;
Matches 99; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSDVDGDSYM-WYQKPGQPPKLLTYAASNLES 59
DB 1 DIQLTQSPASLAVSLGQRATISCKASQSDVDGDSYM-WYQKPGQPPKLLTYAASNLES 60

QY 60 GIPARFSGSGGTDFTLNHPVEEEDAAATYCOLCNEDEPPTFGAGT 105
DB 61 GIPARFSGSGGTDFTLNHPVEEEDAAATYCOLCNEDEPPTFGAGT 106

RESULT 10
US-09-802-077-2
; Sequence 2, Application US/09802077
; Patent No. US20010033842A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C2US
; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 2
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-802-077-2

Query Match      84.5%; Score 491.5; DB 9; Length 111;
Best Local Similarity 88.3%; Pred. No. 1.5e-40;
Matches 98; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSDVDGDSYM-WYQKPGQPPKLLTYAASNLES 59
DB 1 DIQLTQSPASLAVSLGQRATISCKASQSDVDGDSYM-WYQKPGQPPKLLTYAASNLES 60

QY 60 GIPARFSGSGGTDFTLNHPVEEEDAAATYCOLCNEDEPPTFGAGT 110
DB 61 EIPARFSGSGGTDFTLNHPVEEEDAAATYCOLCNEDEPPTFGAGT 111

RESULT 12
US-09-925-179-2
; Sequence 2, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-IGE Antibodies (as amended)
; FILE REFERENCE: P0718P2C1D1C1US
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 2
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-802-077-2

Query Match      84.5%; Score 491.5; DB 9; Length 111;
Best Local Similarity 88.3%; Pred. No. 1.5e-40;
Matches 98; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSDVDGDSYM-WYQKPGQPPKLLTYAASNLES 59
DB 1 DIQLTQSPASLAVSLGQRATISCKASQSDVDGDSYM-WYQKPGQPPKLLTYAASNLES 60

QY 60 GIPARFSGSGGTDFTLNHPVEEEDAAATYCOLCNEDEPPTFGAGT 110
DB 61 EIPARFSGSGGTDFTLNHPVEEEDAAATYCOLCNEDEPPTFGAGT 111

RESULT 11
US-09-802-096-2
; Sequence 2, Application US/09802096
; Patent No. US20010038839A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C3US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 2
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-802-096-2

Query Match      84.5%; Score 491.5; DB 9; Length 111;
Best Local Similarity 88.3%; Pred. No. 1.5e-40;
Matches 98; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSDVDGDSYM-WYQKPGQPPKLLTYAASNLES 59
DB 1 DIQLTQSPASLAVSLGQRATISCKASQSDVDGDSYM-WYQKPGQPPKLLTYAASNLES 60

QY 60 GIPARFSGSGGTDFTLNHPVEEEDAAATYCOLCNEDEPPTFGAGT 110
DB 61 EIPARFSGSGGTDFTLNHPVEEEDAAATYCOLCNEDEPPTFGAGT 111
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; SEQ ID NO 2
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-925-179-2

Query Match      84.5%; Score 491.5; DB 11; Length 111;
Best Local Similarity 88.3%; Pred. No. 1.5e-40;
Matches 98; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSDVDGDSYM-WYQKPGQPPKLLTYAASNLES 59
Db 1 DIVLTQSPGTLSPGERATLSCKASQSDVDGDSYNNWYQKPGQPPKLLTYAASNLES 60
QY 60 GIPARFSGSGGTDFTLNHPVEEEDAATYYCQCNEDPPTFGAGTKLEIK 110
Db 61 EIPARFSGSGGTDFTLNHPVEEEDAATYYCQSHEDPYTFGAGTKLEIK 111

RESULT 13
US-10-160-506-81
; Sequence 81, Application US/10160506
; Publication No. US20030161832A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING
; TITLE OF INVENTION: SKIN DISORDERS USING BINDING AGENTS SPECIFIC FOR
; TITLE OF INVENTION: PROSTATE SPECIFIC MEMBRANE ANTIGEN
; FILE REFERENCE: 10448-182001
; CURRENT APPLICATION NUMBER: US/10/160,506
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/324,100
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/362,612
; PRIOR FILING DATE: 2002-03-08
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-160-506-81

Query Match      84.2%; Score 490; DB 12; Length 112;
Best Local Similarity 85.7%; Pred. No. 2.2e-40;
Matches 96; Conservative 7; Mismatches 7; Indels 2; Gaps 2;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSDVDGDSYM-WYQKPGQPPKLLTYAASNLES 59
Db 1 DIVLTQSPGTLSPGERATISCKASQSDVSGNSFMHWYQKPGQPPKLLTYAASNLES 60
QY 60 GIPARFSGSGGTDFTLNHPVEEEDAATYYCQCNEDPPTFGAGTKLEIK 110
Db 61 GVPARFSGSGGTDFTLNHPVEEEDAATYYCQSNEDPPTFGGTKLEIK 112

RESULT 14
US-10-384-933-54
; Sequence 54, Application US/10384933
; Publication No. US20030170817A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030170817Alufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/384,933
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
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; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 54
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Designed light
; OTHER INFORMATION: chain of humanized anti-Fas antibody
US-10-384-933-54

Query Match      83.8%; Score 487.5; DB 12; Length 238;
Best Local Similarity 83.8%; Pred. No. 8.8e-40;
Matches 93; Conservative 7; Mismatches 10; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSDVDGDSYM-WYQKPGQPPKLLTYAASNLES 59
Db 21 DIVLTQSPGTLSPGERATLSCKASQSDVDGDSYNNWYQKPGQPPKLLTYAASNLES 80
QY 60 GIPARFSGSGGTDFTLNHPVEEEDAATYYCQCNEDPPTFGAGTKLEIK 110
Db 81 GIPDRFSGSGGTDFTLNHPVEEEDAATYYCQSNEDPRTFGGTRLEIK 131

RESULT 15
US-10-216-484-54
; Sequence 54, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030103976Alufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 54
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Designed light
; OTHER INFORMATION: chain of humanized anti-Fas antibody
US-10-216-484-54

Query Match      83.8%; Score 487.5; DB 15; Length 238;
Best Local Similarity 83.8%; Pred. No. 8.8e-40;
Matches 93; Conservative 7; Mismatches 10; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSDVDGDSYM-WYQKPGQPPKLLTYAASNLES 59
Db 21 DIVLTQSPGTLSPGERATLSCKASQSDVDGDSYNNWYQKPGQPPKLLTYAASNLES 80
QY 60 GIPARFSGSGGTDFTLNHPVEEEDAATYYCQCNEDPPTFGAGTKLEIK 110
Db 81 GIPDRFSGSGGTDFTLNHPVEEEDAATYYCQSNEDPRTFGGTRLEIK 131

Search completed: January 14, 2004, 19:25:04
Job time : 153.81 secs
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